



## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al. ) Group Art Unit Unknown  
Appl. No. : 10/017,086 )  
Filed : October 24, 2001 ) I hereby certify that this correspondence and all  
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ACIDS ENCODING THE SAME ) Patents, Washington, D.C. 20231, on  
Examiner : Unknown )  
April 25, 2002  
(Date)  
Ginger R. Dreger, Reg. No. 33,055

SEQUENCE SUBMISSION STATEMENT

Commissioner for Patents  
Washington, D.C. 20231

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed April 2, 2002. I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a) and included in the Substitute Sequence Listing submitted herewith, are supported in the application, and that the Substitute Sequence Listing does not include new matter.

I further state that the information recorded in the currently submitted substitute copy of the computer-readable form of the Sequence Listing is identical to the paper form of the Sequence Listing submitted herewith as required in 37 C.F.R. § 1.825(b).

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: April 25, 2002

By:

Ginger R. Dreger

Registration No. 33,055

Attorney of Record

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Newport Beach, CA 92660

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#5

# Sequence Listing

<110> Ashkenazi, Avi  
Baker Kevin P.  
Botstein, David  
Desnoyers, Luc  
Eaton, Dan  
Ferrara, Napoleon  
Filvaroff, Ellen  
Fong, Sherman  
Gao, Wei-Qiang  
Gerber, Hanspeter  
Gerritsen, Mary E.  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, J. Christopher  
Gurney, Austin L.  
Hillan, Kenneth J.  
Kljavin, Ivar J.  
Kuo, Sophia S.  
Napier, Mary A.  
Pan, James;  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Shelton, David L.  
Stewart, Timothy A.  
Tumas, Daniel  
Williams, P. Mickey  
Wood, William I.

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tagatatatt acctggttct gctatcctta gtcataactc tgcggtacag 2600  
gtaattgaga atgtactacg gtacttcctt cccacaccat acgataaagc 2650  
aagacatttt ataacgatac cagagtcact atgtggctct ccctgaaata 2700  
acgcattcga aatccatgca gtgcagtata tttttctaag ttttgaaag 2750

cagggtttttt cctttaaaaa aattatagac acggttcact aaattgattt 2800  
 agtcagaatt cctagactga aagaacctaa acaaaaaaat atttttaaaga 2850  
 tataaatata tgctgtatat gttatgtaat ttatttttagg ctataataca 2900  
 tttcctatttt tcgcattttc aataaaatgt ctctaataca aaaaa 2945

<210> 7  
 <211> 492  
 <212> PRT  
 <213> Homo sapiens

<400> 7  
 Met Val Lys Phe Pro Ala Leu Thr His Tyr Trp Pro Leu Ile Arg  
 1 5 10 15  
 Phe Leu Val Pro Leu Gly Ile Thr Asn Ile Ala Ile Asp Phe Gly  
 20 25 30  
 Glu Gln Ala Leu Asn Arg Gly Ile Ala Ala Val Lys Glu Asp Ala  
 35 40 45  
 Val Glu Met Leu Ala Ser Tyr Gly Leu Ala Tyr Ser Leu Met Lys  
 50 55 60  
 Phe Phe Thr Gly Pro Met Ser Asp Phe Lys Asn Val Gly Leu Val  
 65 70 75  
 Phe Val Asn Ser Lys Arg Asp Arg Thr Lys Ala Val Leu Cys Met  
 80 85 90

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Val Val Ala Gly Ala Ile Ala Ala Val Phe His Thr Leu Ile Ala  
 95 100 105  
 Tyr Ser Asp Leu Gly Tyr Tyr Ile Ile Asn Lys Leu His His Val  
 110 115 120  
 Asp Glu Ser Val Gly Ser Lys Thr Arg Arg Ala Phe Leu Tyr Leu  
 125 130 135  
 Ala Ala Phe Pro Phe Met Asp Ala Met Ala Trp Thr His Ala Gly  
 140 145 150  
 Ile Leu Leu Lys His Lys Tyr Ser Phe Leu Val Gly Cys Ala Ser  
 155 160 165  
 Ile Ser Asp Val Ile Ala Gln Val Val Phe Val Ala Ile Leu Leu  
 170 175 180  
 His Ser His Leu Glu Cys Arg Glu Pro Leu Leu Ile Pro Ile Leu  
 185 190 195  
 Ser Leu Tyr Met Gly Ala Leu Val Arg Cys Thr Thr Leu Cys Leu  
 200 205 210

Gly Tyr Tyr Lys Asn Ile His Asp Ile Ile Pro Asp Arg Ser Gly	215	220	225
Pro Glu Leu Gly Gly Asp Ala Thr Ile Arg Lys Met Leu Ser Phe	230	235	240
Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
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Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	



<210> 8  
<211> 535  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 66, 96, 387  
<223> unknown base

<400> 8  
cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
tgagcttctg gtgcencttg gctctaattc tggccacaca gagaancagt 100  
cggcctattg tcaacctctt tggttcccg gaccttggtg gcagttctgc 150  
agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
ggccacatc aagaagtcca ccttcgtctg catggctctg tcactcacgc 350  
tctgtttcgt gatgttttgg acaccaacg tgtctngaa aatcttgata 400  
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450  
gcggatcttc tccttcttcc cagttccagt cacagtgagg gcgcatctca 500  
ccgggtggct gatgacactg aagaaaacct tcgtc 535

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<210> 9  
<211> 434  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,  
293, 296, 305, 336, 358, 361  
<223> unknown base

<400> 9  
tgacggaatc ccgggctggg tatcctgggt tngacaagat aaacccccag 50  
caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100  
agttcacctt ngtttgnatg gntctgtcaa ctcacgctnt gtttcgtgat 150  
gttttgagca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200  
tggantttgc ctttgagaa ntttgngntg ttcctttgcg gatcttctcc 250  
tttttccag ttccagtcac agngagggcg catctcaccg gngngntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350  
ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400  
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10  
<211> 154  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 33, 49, 68, 83, 90, 98, 119  
<223> unknown base

<400> 10  
tattcccagt tccggtcacg gggagggcgc atntcacggg gtggctgang 50  
aactgaaga aaaccttngt ccttgcccc agntttgtgn tgcggatnat 100  
cgctctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150  
agac 154

<210> 11  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattcttcc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgccg cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgtc 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 16  
gcctgctgtg gtcacaggtc tccg 24

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<210> 17  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 17  
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18  
<211> 1901  
<212> DNA  
<213> Homo sapiens

<400> 18  
gccccgcgcc cggcgcggg cgcccgaagc cgggagccac cgccatgggg 50  
gcctgcctgg gagcctgtc cctgtcagc tgcggtcct gcctctgcgg 100  
ctctgcccc tgcactctgt gcagctgtg ccccgccagc cgcaactcca 150

ccgtgagccg cctcatcttc acgttcttcc tcttcctggg ggtgctggtg 200  
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250  
ctgggtgtgt gaggaggggg ccgggatccc caccgtcctg cagggccaca 300  
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350  
gccacggcgg ccttcttctt cttctttttc accctgctca tgctctgcgt 400  
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450  
ttaagttcct gatcctggtg ggctcaccg tgggtgcctt ctacatccct 500  
gacggctcct tcaccaacat ctggttctac ttcggcgtcg tgggctcctt 550  
cctcttcctc ctcatccagc tgggtgctgct catcgacttt gcgcactcct 600  
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650  
tacgcaggcc tcttcttctt cactctctc ttctacttgc tgcgatcgc 700  
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750  
agggaagggt cttcatcagc ctcaacctca cttctgtgt ctgctgtcc 800  
atcgtgctg tctgcccac ggtccaggac gccagccca actcgggtct 850  
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900  
ccctatccag tatccctgaa cagaaatgca accccattt gccaacccag 950  
ctgggcaacg agacagtgtt ggcaggcccc gagggctatg agaccagtg 1000

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gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050  
tcttcatcag tctgcgtcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150  
gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactcctt ttccacttct gcctgggtgct ggctcactg 1250  
cacgtcatga tgacgtcac caactggtac aagcccgtg agaccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
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aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450  
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caccaatcag ccaggctgag cccccacccc tgcccagct ccaggacctg 1550  
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caggctcctg cagagcccca tcccccgcc acaccacac ggtggagctg 1650  
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 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctgggtgttc 1800  
 tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850  
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900  
 a 1901

<210> 19  
 <211> 457  
 <212> PRT  
 <213> Homo sapiens

<400> 19  
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser  
 1 5 10 15  
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
 20 25 30  
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
 35 40 45  
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
 50 55 60

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Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly  
 65 70 75  
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser  
 80 85 90  
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala  
 95 100 105  
 Ala Phe Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser  
 110 115 120  
 Ser Ser Arg Asp Pro Arg Ala Ala Ile Gln Asn Gly Phe Trp Phe  
 125 130 135  
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr  
 140 145 150  
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val  
 155 160 165  
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile  
 170 175 180

Asp	Phe	Ala	His	Ser 185	Trp	Asn	Gln	Arg	Trp 190	Leu	Gly	Lys	Ala	Glu 195
Glu	Cys	Asp	Ser	Arg 200	Ala	Trp	Tyr	Ala	Gly 205	Leu	Phe	Phe	Phe	Thr 210
Leu	Leu	Phe	Tyr	Leu 215	Leu	Ser	Ile	Ala	Ala 220	Val	Ala	Leu	Met	Phe 225
Met	Tyr	Tyr	Thr	Glu 230	Pro	Ser	Gly	Cys	His 235	Glu	Gly	Lys	Val	Phe 240
Ile	Ser	Leu	Asn	Leu 245	Thr	Phe	Cys	Val	Cys 250	Val	Ser	Ile	Ala	Ala 255
Val	Leu	Pro	Lys	Val 260	Gln	Asp	Ala	Gln	Pro 265	Asn	Ser	Gly	Leu	Leu 270
Gln	Ala	Ser	Val	Ile 275	Thr	Leu	Tyr	Thr	Met 280	Phe	Val	Thr	Trp	Ser 285
Ala	Leu	Ser	Ser	Ile 290	Pro	Glu	Gln	Lys	Cys 295	Asn	Pro	His	Leu	Pro 300
Thr	Gln	Leu	Gly	Asn 305	Glu	Thr	Val	Val	Ala 310	Gly	Pro	Glu	Gly	Tyr 315
Glu	Thr	Gln	Trp	Trp 320	Asp	Ala	Pro	Ser	Ile 325	Val	Gly	Leu	Ile	Ile 330
Phe	Leu	Leu	Cys	Thr 335	Leu	Phe	Ile	Ser	Leu 340	Arg	Ser	Ser	Asp	His 345
Arg	Gln	Val	Asn	Ser 350	Leu	Met	Gln	Thr	Glu 355	Glu	Cys	Pro	Pro	Met 360
Leu	Asp	Ala	Thr	Gln 365	Gln	Gln	Gln	Gln	Gln 370	Val	Ala	Ala	Cys	Glu 375
Gly	Arg	Ala	Phe	Asp 380	Asn	Glu	Gln	Asp	Gly 385	Val	Thr	Tyr	Ser	Tyr 390
Ser	Phe	Phe	His	Phe 395	Cys	Leu	Val	Leu	Ala 400	Ser	Leu	His	Val	Met 405
Met	Thr	Leu	Thr	Asn 410	Trp	Tyr	Lys	Pro	Gly 415	Glu	Thr	Arg	Lys	Met 420
Ile	Ser	Thr	Trp	Thr 425	Ala	Val	Trp	Val	Lys 430	Ile	Cys	Ala	Ser	Trp 435
Ala	Gly	Leu	Leu	Leu 440	Tyr	Leu	Trp	Thr	Leu 445	Val	Ala	Pro	Leu	Leu 450
Leu	Arg	Asn	Arg	Asp 455	Phe	Ser								

<210> 20  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 20  
gccgcctcat cttcacgttc ttcc 24

<210> 21  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 21  
tcattccagct ggtgctgctc 20

<210> 22  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 22  
cttcttccac ttctgctg 20

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<210> 23  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcaccc acgg 24

<210> 25  
<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 25

tgccacagat cttcaccac acgg 24

<210> 26

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 26

tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27

<211> 1351

<212> DNA

<213> Homo sapiens

<400> 27

gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50

ttaacctggg tcaaatgcac ggattctcac ctcgtagagt tacgtctctc 100

cgcggcacgt ccgcgaggac ttgaagtctt gagcgctcaa gtttgtccgt 150

aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200

tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300

cccagagccc tattaccgg aatctggatg ggaccgctc cgggagctgt 350

ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400

aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450

agcttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500

tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550

cgaggcttca ttcgttatgg ctggcgctgg ggttgagaa ctgcagtgtt 600

tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650

aagatgcctt aagccatttt gtaattgcag gagctgtcac ggggaagtctt 700

tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750

agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800



acgctgggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
 catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
 cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950  
 atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000  
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 aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350  
 t 1351

<210> 28  
 <211> 285  
 <212> PRT  
 <213> Homo sapiens

<400> 28

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1				5					10					15

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Leu	Cys	Leu	Phe	Pro	Arg	Val	Phe	Ala	Ala	Glu	Ala	Val	Thr	Ala
				20					25					30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val
				35					40					45

Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu
				50					55					60

Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala
				65					70					75

Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val
				80					85					90

Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile
				95					100					105

Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val
				110					115					120

Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly
				125					130					135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattacccg gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250

ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300

ttcgttcattg gctggcgccg aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure  
<222> 262, 330, 371  
<223> unknown base

<400> 30  
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50  
accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
agagccaggc agaaatttat nataacc 377

<210> 31  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 31  
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<210> 32  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaataatct gtaagacggc agctacagca ggcattcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgcccgc cgcgcgcgcgc cgcgcgcactg cagccccagg ccccggcccc 50

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tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200

aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgct 250

gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300

tccgagtggc cggcgtggtc attgcagtgg gcatcttctt gttcctgatt 350

gcttttagtggt gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400

tttttatatg attattctgt tacttgtatt tattgttcag ttttctgtat 450

cttgcgcttg ttagccctg aaccaggagc aacaggggtca gcttctggag 500

gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550

aaactgctgt gggttccgaa gtgttaacct aaatgacacc tgtctggcta 600

gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650

gaatatgctg gagaggtttt gagatttggt ggtggcattg gcctgttctt 700

cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750

agaaagaccc cgcgcgcaat cctagtgcac tcctttgatg agaaaacaag 800

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 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800  
 taaaagaaag taatggaag 1819

<210> 36

<211> 204

<212> PRT

<213> Homo sapiens

<400> 36

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				20					25					30	
Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val	
				35					40					45	
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala	
				50					55					60	
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu	
				65					70					75	
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe	
				80					85					90	
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly	
				95					100					105	

Gln Leu Leu Glu Val Gly Trp Asn Asn Thr Ala Ser Ala Arg Asn  
 110 115 120  
 Asp Ile Gln Arg Asn Leu Asn Cys Cys Gly Phe Arg Ser Val Asn  
 125 130 135  
 Pro Asn Asp Thr Cys Leu Ala Ser Cys Val Lys Ser Asp His Ser  
 140 145 150  
 Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu Tyr Ala Gly Glu Val  
 155 160 165  
 Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe Ser Phe Thr Glu  
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 185 190 195  
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<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

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 tagccntgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300  
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 gatcctgggt gtttggtgta cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27

<223> unknown base

<400> 38

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tttttgactt ttacaggtaa gtgcaaagga gaagtggttt catgaaatgt 200  
tctaattgat aataacattt accttcagcc tcccatcaga atggaacgag 250  
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
gcatatttga atatgatctc ccataatttg aaattgaaat cgtattgtgt 500  
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gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

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tggttggaac caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
aatcctaaac tgctgtgggt tccgaagtgt taaccctaat gacacctgtc 200  
tggtctngctg tggtaaaagt gaccactcgt gctcgccatg tgctccaatc 250  
ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40  
accacgtct gcgttgctgc c 21

<210> 41  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 41  
gagaatatgc tggagagg 18

<210> 42  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 42  
aggaatgcac taggattcgc gcgg 24

<210> 43  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
~~<223> Synthetic oligonucleotide probe~~

<400> 43  
ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44  
<211> 2061  
<212> DNA  
<213> Homo sapiens

<400> 44  
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gacgctgcag tgtgaggac ctgtctgcac tgaggagagc agctgccaca 150  
cggaggatga cttgactgat gcaagggaag ctggcttcca ggtcaaggcc 200  
tacactttca gtgaaccctt ccacctgatt gtgtcctatg actggctgat 250  
cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300  
gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350



gatggctcag ctctgggtcc ccccgggcct aacagggaat tctccatcac 400  
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acccaagca ggaagcccca tgaccctgag ttgtcagaca aagttgcccc 600  
tgcagaggtc agctgccgc ctctcttct cttctacaa ggatggaagg 650  
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agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
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 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgccaac accgactctg tcgttgccctt 2000  
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 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

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 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75

Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150  
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val  
 155 160 165  
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala  
 170 175 180  
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys  
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

<210> 46  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 46  
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<210> 47  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 47  
 tttccagcgc caattctc 18

<210> 48

<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcctcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
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<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
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 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
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<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
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 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75

His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
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 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180  
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr  
 185 190 195

Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser Tyr Phe  
 200 205 210  
 Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp Ile  
 215 220 225  
 Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys  
 230 235 240  
 Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser  
 245 250 255  
 Thr Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr  
 260 265 270  
 Leu Gly Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe  
 275 280 285  
 Ala Ile Ile Leu Ile Ile Ser Leu Cys Cys Met Val Val Phe Thr  
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<210> 53

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 53

tatccctcca attgagcacc ctgg 24

<210> 54

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 54

gtcgggaagac atcccaacaa g 21

<210> 55

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55  
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<210> 56  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 56  
agccaaatcc agcagctggc ttac 24

<210> 57  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 57  
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<210> 58  
<211> 2458  
<212> DNA  
<213> Homo sapiens

<400> 58  
gcgccgggag cccatctgcc cccaggggca cggggcgcg ggcgggctcc 50

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<211> 373

<212> PRT

<213> Homo sapiens

<400> 59

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Thr	Leu	Gly	Thr	His	Thr	Glu	Ile	Lys	Arg	Val	Ala	Glu	Glu	Lys
				20					25					30

Val	Thr	Leu	Pro	Cys	His	His	Gln	Leu	Gly	Leu	Pro	Glu	Lys	Asp
				35					40					45

Thr	Leu	Asp	Ile	Glu	Trp	Leu	Leu	Thr	Asp	Asn	Glu	Gly	Asn	Gln
				50					55					60

Lys	Val	Val	Ile	Thr	Tyr	Ser	Ser	Arg	His	Val	Tyr	Asn	Asn	Leu
				65					70					75

Thr	Glu	Glu	Gln	Lys	Gly	Arg	Val	Ala	Phe	Ala	Ser	Asn	Phe	Leu
				80					85					90

Ala	Gly	Asp	Ala	Ser	Leu	Gln	Ile	Glu	Pro	Leu	Lys	Pro	Ser	Asp
				95					100					105

Glu	Gly	Arg	Tyr	Thr	Cys	Lys	Val	Lys	Asn	Ser	Gly	Arg	Tyr	Val
				110					115					120

Trp	Ser	His	Val	Ile	Leu	Lys	Val	Leu	Val	Arg	Pro	Ser	Lys	Pro
				125					130					135

Lys	Cys	Glu	Leu	Glu	Gly	Glu	Leu	Thr	Glu	Gly	Ser	Asp	Leu	Thr
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Leu	Gln	Cys	Glu	Ser	Ser	Ser	Gly	Thr	Glu	Pro	Ile	Val	Tyr	Tyr
				155					160					165

Trp	Gln	Arg	Ile	Arg	Glu	Lys	Glu	Gly	Glu	Asp	Glu	Arg	Leu	Pro
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170	175	180
Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu	
185	190	195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala	
200	205	210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val	
215	220	225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly	
230	235	240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu	
245	250	255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro	
260	265	270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val	
275	280	285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly	
290	295	300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln	
305	310	315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr	
320	325	330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro	
335	340	345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro	
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Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val	
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggctgt atgcctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 62

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<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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<210> 64

<211> 655

<212> PRT

<213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

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Gln Gln Gly Pro	His His Arg His Ile	Leu Lys Leu Leu Pro	Ser
305		310	315
Met Glu Ala Thr	Gly Gly Glu Lys Ser	Ser Thr Pro Ile Lys	Gly
320		325	330
Pro Lys Arg Gly	His Pro Arg Gln Asn	Leu His Lys His Phe	Asp
335		340	345
Ile Asn Glu His	Leu Pro Trp Met Ile	Val Leu Phe Leu Leu	Leu
350		355	360
Val Leu Val Val	Ile Val Val Cys Ser	Ile Arg Lys Ser Ser	Arg
365		370	375
Thr Leu Lys Lys	Gly Pro Arg Gln Asp	Pro Ser Ala Ile Val	Glu
380		385	390
Lys Ala Gly Leu	Lys Lys Ser Met Thr	Pro Thr Gln Asn Arg	Glu
395		400	405
Lys Trp Ile Tyr	Tyr Cys Asn Gly His	Gly Ile Asp Ile Leu	Lys
410		415	420
Leu Val Ala Ala	Gln Val Gly Ser Gln	Trp Lys Asp Ile Tyr	Gln
425		430	435
Phe Leu Cys Asn	Ala Ser Glu Arg Glu	Val Ala Ala Phe Ser	Asn
440		445	450
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Ala Leu Arg Gln	His Arg Arg Asn Asp	Val Val Glu Lys Ile	Arg
485		490	495
Gly Leu Met Glu	Asp Thr Thr Gln Leu	Glu Thr Asp Lys Leu	Ala
500		505	510
Leu Pro Met Ser	Pro Ser Pro Leu Ser	Pro Ser Pro Ile Pro	Ser
515		520	525
Pro Asn Ala Lys	Leu Glu Asn Ser Ala	Leu Leu Thr Val Glu	Pro
530		535	540
Ser Pro Gln Asp	Lys Asn Lys Gly Phe	Phe Val Asp Glu Ser	Glu
545		550	555
Pro Leu Leu Arg	Cys Asp Ser Thr Ser	Ser Gly Ser Ser Ala	Leu
560		565	570



Ser Arg Asn Gly Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr Val  
575 580 585

Leu Arg Gln Val Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile Phe  
590 595 600

Asp Asp Met Leu His Phe Leu Asn Pro Glu Glu Leu Arg Val Ile  
605 610 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
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Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
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Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
650 655

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 65

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<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

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ttccctcatt gtctggcgtg tctgcgtgga ctggtgacgt gaatcaaaat 2400  
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<210> 69

<211> 453

<212> PRT

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20					25					30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35					40					45

Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile

50					55					60				
Leu	Ala	Leu	Ala	Ile	Gly	Leu	Gly	Ile	His	Phe	Asp	Cys	Ser	Gly
				65					70					75
Lys	Tyr	Arg	Cys	Arg	Ser	Ser	Phe	Lys	Cys	Ile	Glu	Leu	Ile	Ala
				80					85					90
Arg	Cys	Asp	Gly	Val	Ser	Asp	Cys	Lys	Asp	Gly	Glu	Asp	Glu	Tyr
				95					100					105
Arg	Cys	Val	Arg	Val	Gly	Gly	Gln	Asn	Ala	Val	Leu	Gln	Val	Phe
				110					115					120
Thr	Ala	Ala	Ser	Trp	Lys	Thr	Met	Cys	Ser	Asp	Asp	Trp	Lys	Gly
				125					130					135
His	Tyr	Ala	Asn	Val	Ala	Cys	Ala	Gln	Leu	Gly	Phe	Pro	Ser	Tyr
				140					145					150
Val	Ser	Ser	Asp	Asn	Leu	Arg	Val	Ser	Ser	Leu	Glu	Gly	Gln	Phe
				155					160					165
Arg	Glu	Glu	Phe	Val	Ser	Ile	Asp	His	Leu	Leu	Pro	Asp	Asp	Lys
				170					175					180
Val	Thr	Ala	Leu	His	His	Ser	Val	Tyr	Val	Arg	Glu	Gly	Cys	Ala
				185					190					195
Ser	Gly	His	Val	Val	Thr	Leu	Gln	Cys	Thr	Ala	Cys	Gly	His	Arg
				200					205					210
Arg	Gly	Tyr	Ser	Ser	Arg	Ile	Val	Gly	Gly	Asn	Met	Ser	Leu	Leu
				215					220					225
Ser	Gln	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Gln	Phe	Gln	Gly	Tyr	His
				230					235					240
Leu	Cys	Gly	Gly	Ser	Val	Ile	Thr	Pro	Leu	Trp	Ile	Ile	Thr	Ala
				245					250					255
Ala	His	Cys	Val	Tyr	Asp	Leu	Tyr	Leu	Pro	Lys	Ser	Trp	Thr	Ile
				260					265					270
Gln	Val	Gly	Leu	Val	Ser	Leu	Leu	Asp	Asn	Pro	Ala	Pro	Ser	His
				275					280					285
Leu	Val	Glu	Lys	Ile	Val	Tyr	His	Ser	Lys	Tyr	Lys	Pro	Lys	Arg
				290					295					300
Leu	Gly	Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Ala	Gly	Pro	Leu	Thr
				305					310					315
Phe	Asn	Glu	Met	Ile	Gln	Pro	Val	Cys	Leu	Pro	Asn	Ser	Glu	Glu
				320					325					330
Asn	Phe	Pro	Asp	Gly	Lys	Val	Cys	Trp	Thr	Ser	Gly	Trp	Gly	Ala

335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala		
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys Asn His Arg Asp Val Tyr		
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu Cys Ala Gly Tyr Leu Thr		
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val		
395	400	405
Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe		
410	415	420
Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg		
425	430	435
Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp		
440	445	450
Leu Lys Thr		

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

tgacatcgcc cttatgaagc tggc 24

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

tacacgtccc tgtggttgca gatc 24

<210> 72

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 72

cgttcaatgc agaaatgatc cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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gaaat 3305

<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
				20					25					30
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
				35					40					45
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp
				50					55					60
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
				65					70					75
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80					85					90
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
				95					100					105
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
				110					115					120



His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
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Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly  
410 415 420

Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys  
425 430 435

Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala  
440 445 450

Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu  
455 460 465

Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg  
470 475 480

Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala  
485 490 495

Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser  
500 505 510

Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr  
515 520 525

His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro  
530 535 540

Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro  
545 550 555

Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys  
560 565 570

Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly  
575 580 585

Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr  
590 595 600

Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr  
605 610 615

His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu  
620 625 630

Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln  
635 640 645

Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln  
650 655 660

Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys  
665 670 675

Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly  
680 685 690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln  
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro  
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile  
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctaccagga agtttgcaga aacagtgcaa ggaagggcag ganttcctgg 150

ttgagntttt tgntaaaaca tggacatgnt tcagtgtctgc tcntgagaga 200

gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

agcaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

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<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 77  
catgagcatg tgcacggc 18

<210> 78  
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<212> DNA  
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<220>  
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<400> 78  
tacctgcacg atgggcac 18

<210> 79  
<211> 18  
<212> DNA  
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<220>  
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<400> 79  
cactgggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
<213> Artificial Sequence

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<220>  
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<400> 80  
ctccaggctg gtctccaagt ccttcc 26

<210> 81  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
tccctggttg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagtttg 19

<210> 83  
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<210> 84  
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<212> DNA  
<213> Homo sapiens

<400> 84  
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atgatctgcc cgctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
ctggatacaa aagtacaatc ttactgtgt aaatacatgt atatgtacta 300  
tatgaaaata taccaaatat caataaact tatctctggg taaaaacctc 350  
ttctcatacc ctgtgctaac aacttttaac aaaaaatttg catcactttt 400  
aagaatcaag aaaaatttct gaaggtcata tgggacagaa aaaaaaacca 450  
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<210> 85  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

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 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
 35 40 45  
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
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<210> 86  
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<212> DNA  
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<220>  
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<400> 86  
acgggcacac tggatcccaa atg 23

<210> 87  
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ggtagagatg tagaaggga agcaagacc 29

<210> 88  
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<212> DNA  
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<210> 89  
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<212> DNA  
<213> Homo sapiens

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 <213> Homo sapiens

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 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45

Ala	Asp	Gly	Pro	Pro	Ala	Ala	Asp	Gly	Glu	Asp	Gly	Gln	Asp	Pro	
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His	Ser	Lys	His	Leu	Tyr	Thr	Ala	Asp	Met	Phe	Thr	His	Gly	Ile	
				65					70					75	
Gln	Ser	Ala	Ala	His	Phe	Val	Met	Phe	Phe	Ala	Pro	Trp	Cys	Gly	
				80					85					90	
His	Cys	Gln	Arg	Leu	Gln	Pro	Thr	Trp	Asn	Asp	Leu	Gly	Asp	Lys	
				95					100					105	
Tyr	Asn	Ser	Met	Glu	Asp	Ala	Lys	Val	Tyr	Val	Ala	Lys	Val	Asp	
				110					115					120	
Cys	Thr	Ala	His	Ser	Asp	Val	Cys	Ser	Ala	Gln	Gly	Val	Arg	Gly	
				125					130					135	
Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Lys	Pro	Gly	Gln	Glu	Ala	Val	Lys	
				140					145					150	
Tyr	Gln	Gly	Pro	Arg	Asp	Phe	Gln	Thr	Leu	Glu	Asn	Trp	Met	Leu	
				155					160					165	
Gln	Thr	Leu	Asn	Glu	Glu	Pro	Val	Thr	Pro	Glu	Pro	Glu	Val	Glu	
				170					175					180	
Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	
				185					190					195	
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	
				200					205					210	

Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	
				215					220					225	
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	
				230					235					240	
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	
				245					250					255	
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	
				260					265					270	
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	
				275					280					285	
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	
				290					295					300	
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	
				305					310					315	
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	
				320					325					330	

Asn Phe Asp Asp Thr Ile Ala Glu Gly Ile Thr Phe Ile Lys Phe  
335 340 345

Tyr Ala Pro Trp Cys Gly His Cys Lys Thr Leu Ala Pro Thr Trp  
350 355 360

Glu Glu Leu Ser Lys Lys Glu Phe Pro Gly Leu Ala Gly Val Lys  
365 370 375

Ile Ala Glu Val Asp Cys Thr Ala Glu Arg Asn Ile Cys Ser Lys  
380 385 390

Tyr Ser Val Arg Gly Tyr Pro Thr Leu Leu Leu Phe Arg Gly Gly  
395 400 405

Lys Lys Val Ser Glu His Ser Gly Gly Arg Asp Leu Asp Ser Leu  
410 415 420

His Arg Phe Val Leu Ser Gln Ala Lys Asp Glu Leu  
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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<400> 92  
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<212> DNA  
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<220>  
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<400> 93  
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<210> 94  
<211> 23

<212> DNA  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
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<210> 96  
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<212> DNA  
<213> Homo sapiens

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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150  
atttcaccag gacccaaagg agatgatggg gaaaaaggag atccaggaga 200

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 cagttattgt tatccatcct ttttttcctg attgtactac atttgatctg 950  
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<210> 97  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 97  
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 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
 35 40 45  
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
 50 55 60  
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
 65 70 75  
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys  
 80 85 90  
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu  
 95 100 105  
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp  
 110 115 120  
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile  
 125 130 135  
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala  
 140 145 150  
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu  
 155 160 165  
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly  
 170 175 180  
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile  
 185 190 195  
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

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Val Asn Asp Leu	Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp	Asn
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Thr Pro Leu Gln	Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro	Ser
	230	235	240
Asp Pro Tyr Gly	His Glu Asp Cys Val	Glu Met Leu Ser Ser	Gly
	245	250	255
Arg Trp Asn Asp	Thr Glu Cys His Leu	Thr Met Tyr Phe Val	Cys
	260	265	270
Glu Phe Ile Lys	Lys Lys Lys		
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<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 98

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<210> 99

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

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<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

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<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

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gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200  
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<210> 102  
<211> 730  
<212> PRT  
<213> Homo sapiens

<400> 102  
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Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly  
20 25 30



Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala  
35 40 45

Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu  
50 55 60

Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
65 70 75

Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
80 85 90

Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
95 100 105

Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
110 115 120

Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
125 130 135

Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
140 145 150

Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
155 160 165

Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
170 175 180

Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
185 190 195

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Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro  
200 205 210

Leu Ser Pro Gly Ala Thr Val Ala Leu Leu Leu Pro Ala Gly Pro  
215 220 225

Glu Phe Leu Trp Leu Trp Phe Gly Leu Ala Lys Ala Gly Leu Arg  
230 235 240

Thr Ala Phe Val Pro Thr Ala Leu Arg Arg Gly Pro Leu Leu His  
245 250 255

Cys Leu Arg Ser Cys Gly Ala Arg Ala Leu Val Leu Ala Pro Glu  
260 265 270

Phe Leu Glu Ser Leu Glu Pro Asp Leu Pro Ala Leu Arg Ala Met  
275 280 285

Gly Leu His Leu Trp Ala Ala Gly Pro Gly Thr His Pro Ala Gly  
290 295 300

Ile Ser Asp Leu Leu Ala Glu Val Ser Ala Glu Val Asp Gly Pro  
305 310 315

Val Pro Gly Tyr Leu Ser Ser Pro Gln Ser Ile Thr Asp Thr Cys  
320 325 330

Leu Tyr Ile Phe Thr Ser Gly Thr Thr Gly Leu Pro Lys Ala Ala  
335 340 345

Arg Ile Ser His Leu Lys Ile Leu Gln Cys Gln Gly Phe Tyr Gln  
350 355 360

Leu Cys Gly Val His Gln Glu Asp Val Ile Tyr Leu Ala Leu Pro  
365 370 375

Leu Tyr His Met Ser Gly Ser Leu Leu Gly Ile Val Gly Cys Met  
380 385 390

Gly Ile Gly Ala Thr Val Val Leu Lys Ser Lys Phe Ser Ala Gly  
395 400 405

Gln Phe Trp Glu Asp Cys Gln Gln His Arg Val Thr Val Phe Gln  
410 415 420

Tyr Ile Gly Glu Leu Cys Arg Tyr Leu Val Asn Gln Pro Pro Ser  
425 430 435

Lys Ala Glu Arg Gly His Lys Val Arg Leu Ala Val Gly Ser Gly  
440 445 450

Leu Arg Pro Asp Thr Trp Glu Arg Phe Val Arg Arg Phe Gly Pro  
455 460 465

Leu Gln Val Leu Glu Thr Tyr Gly Leu Thr Glu Gly Asn Val Ala  
470 475 480

Thr Ile Asn Tyr Thr Gly Gln Arg Gly Ala Val Gly Arg Ala Ser  
485 490 495

Trp Leu Tyr Lys His Ile Phe Pro Phe Ser Leu Ile Arg Tyr Asp  
500 505 510

Val Thr Thr Gly Glu Pro Ile Arg Asp Pro Gln Gly His Cys Met  
515 520 525

Ala Thr Ser Pro Gly Glu Pro Gly Leu Leu Val Ala Pro Val Ser  
530 535 540

Gln Gln Ser Pro Phe Leu Gly Tyr Ala Gly Gly Pro Glu Leu Ala  
545 550 555

Gln Gly Lys Leu Leu Lys Asp Val Phe Arg Pro Gly Asp Val Phe  
560 565 570

Phe Asn Thr Gly Asp Leu Leu Val Cys Asp Asp Gln Gly Phe Leu  
575 580 585

Arg Phe His Asp Arg Thr Gly Asp Thr Phe Arg Trp Lys Gly Glu  
590 595 600

Asn	Val	Ala	Thr	Thr	Glu	Val	Ala	Glu	Val	Phe	Glu	Ala	Leu	Asp	
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Phe	Leu	Gln	Glu	Val	Asn	Val	Tyr	Gly	Val	Thr	Val	Pro	Gly	His	
				620					625					630	
Glu	Gly	Arg	Ala	Gly	Met	Ala	Ala	Leu	Val	Leu	Arg	Pro	Pro	His	
				635					640					645	
Ala	Leu	Asp	Leu	Met	Gln	Leu	Tyr	Thr	His	Val	Ser	Glu	Asn	Leu	
				650					655					660	
Pro	Pro	Tyr	Ala	Arg	Pro	Arg	Phe	Leu	Arg	Leu	Gln	Glu	Ser	Leu	
				665					670					675	
Ala	Thr	Thr	Glu	Thr	Phe	Lys	Gln	Gln	Lys	Val	Arg	Met	Ala	Asn	
				680					685					690	
Glu	Gly	Phe	Asp	Pro	Ser	Thr	Leu	Ser	Asp	Pro	Leu	Tyr	Val	Leu	
				695					700					705	
Asp	Gln	Ala	Val	Gly	Ala	Tyr	Leu	Pro	Leu	Thr	Thr	Ala	Arg	Tyr	
				710					715					720	
Ser	Ala	Leu	Leu	Ala	Gly	Asn	Leu	Arg	Ile						
				725					730						

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 <212> DNA  
 <213> Artificial Sequence

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<210> 104  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 104  
 ggagaatgtg gccacaac 18

<210> 105  
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<220>  
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<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
<211> 18  
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<220>  
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<400> 106  
atccacttca gcggacac 18

<210> 107  
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<400> 107  
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

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Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys
				20					25					30

Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala
				35					40					45

Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys
				50					55					60

Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu
				65					70					75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr
				80					85					90

Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe
				95					100					105

Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120

Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn
				125					130					135

Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp  
155 160 165

Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr  
170 175 180

His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp  
185 190 195

Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln  
200 205 210

Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu  
215 220 225

Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro  
230 235 240

Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro  
245 250 255

Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys  
260 265 270

Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp  
275 280 285

Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu  
290 295 300

Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile  
305 310 315

Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser  
320 325 330

Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys  
335 340 345

Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe  
350 355 360

Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr  
365 370 375

Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu  
380 385 390

Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr  
395 400 405

Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu  
410 415 420

Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile  
425 430 435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 110

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<210> 111

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 111

tgacacgtct ctgcagtgcc cagg 24

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgctg 40



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<211> 4649  
<212> DNA  
<213> Homo sapiens

<400> 113  
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 <211> 515  
 <212> PRT  
 <213> Homo sapiens

<400> 114

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				20					25					30

Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser
				35					40					45

Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala
				50					55					60

Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln
				65					70					75

Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp
				80					85					90

Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys
				95					100					105

Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro
				110					115					120

Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln
				125					130					135

Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro
				140					145					150

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155 160 165

Glu Val Gly Tyr Ser Thr His Met Val Gly Lys Trp His Leu Gly  
170 175 180

Phe Asn Arg Lys Glu Cys Met Pro Thr Arg Arg Gly Phe Asp Thr  
185 190 195

Phe Phe Gly Ser Leu Leu Gly Ser Gly Asp Tyr Tyr Thr His Tyr  
200 205 210

Lys Cys Asp Ser Pro Gly Met Cys Gly Tyr Asp Leu Tyr Glu Asn  
215 220 225

Asp Asn Ala Ala Trp Asp Tyr Asp Asn Gly Ile Tyr Ser Thr Gln  
230 235 240

Met Tyr Thr Gln Arg Val Gln Gln Ile Leu Ala Ser His Asn Pro  
245 250 255

Thr Lys Pro Ile Phe Leu Tyr Thr Ala Tyr Gln Ala Val His Ser  
260 265 270

Pro Leu Gln Ala Pro Gly Arg Tyr Phe Glu His Tyr Arg Ser Ile  
275 280 285

Ile Asn Ile Asn Arg Arg Arg Tyr Ala Ala Met Leu Ser Cys Leu  
290 295 300

Asp Glu Ala Ile Asn Asn Val Thr Leu Ala Leu Lys Thr Tyr Gly  
305 310 315

Phe Tyr Asn Asn Ser Ile Ile Ile Tyr Ser Ser Asp Asn Gly Gly  
320 325 330

Gln Pro Thr Ala Gly Gly Ser Asn Trp Pro Leu Arg Gly Ser Lys  
335 340 345

Gly Thr Tyr Trp Glu Gly Gly Ile Arg Ala Val Gly Phe Val His  
350 355 360

Ser Pro Leu Leu Lys Asn Lys Gly Thr Val Cys Lys Glu Leu Val  
365 370 375

His Ile Thr Asp Trp Tyr Pro Thr Leu Ile Ser Leu Ala Glu Gly  
380 385 390

Gln Ile Asp Glu Asp Ile Gln Leu Asp Gly Tyr Asp Ile Trp Glu  
395 400 405

Thr Ile Ser Glu Gly Leu Arg Ser Pro Arg Val Asp Ile Leu His  
410 415 420

Asn Ile Asp Pro Tyr Thr Pro Arg Gln Lys Met Ala Pro Gly Gln  
425 430 435

Gln Ala Met Gly Ser Gly Thr Leu Gln Ser Ser Gln Pro Ser Glu  
440 445 450

Cys Ser Thr Gly Asn Cys Leu Gln Glu Ile Leu Ala Thr Ala Thr  
455 460 465

Gly Ser Pro Leu Ser Leu Ser Ala Thr Trp Asp Arg Thr Gly Gly  
470 475 480

Thr Met Asn Gly Ser Pro Cys Gln Leu Ala Lys Val Tyr Gly Phe  
485 490 495

Ser Thr Ser Gln Pro Thr His Met Arg Gly Trp Thr Tyr Leu Thr  
500 505 510

Gly Ile Gln Glu Ser  
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<211> 24

<212> DNA

<213> Artificial Sequence

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<400> 115

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<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

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<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

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<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
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Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr		35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val		50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val		65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr		80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys		95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys		110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser		125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr		140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu		155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser		170	175	180
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Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe		185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr		200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met		215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln		230	235	240
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly		245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu		260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala		275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr		290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro  
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Gly Lys Lys Gly Asn Glu Glu Lys  
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<213> Artificial Sequence

<220>

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<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

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<400> 122

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<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

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				20					25					30

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40					45

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55					60

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val			
				65						70				75			
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly			
				80					85					90			
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr			
				95					100					105			
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr			
				110					115					120			
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile			
				125					130					135			
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser			
				140					145					150			
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn			
				155					160					165			
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser			
				170					175					180			
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Glu	Asn	Ser			
				185					190					195			
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln			
				200					205					210			
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile			
				215					220					225			

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Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro			
				230					235					240			
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala			
				245					250					255			
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe			
				260					265					270			
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys			
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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ctgtagacat ccaagctggt atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 129

aagagtctgc atccacacca ctc 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<211> 2365  
<212> DNA  
<213> Homo sapiens

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<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
				20					25					30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser	Leu Met Trp Leu Ser Phe	
35	40	45	
Arg Lys Val Gln Glu	Pro Gln Gly Lys Ala	Lys Arg His Gly Asn	
50	55	60	
Thr Val Pro Gly Glu	Trp Pro Trp Gln Ala	Ser Val Arg Arg Gln	
65	70	75	
Gly Ala His Ile Cys	Ser Gly Ser Leu Val	Ala Asp Thr Trp Val	
80	85	90	
Leu Thr Ala Ala His	Cys Phe Glu Lys Ala	Ala Ala Thr Glu Leu	
95	100	105	
Asn Ser Trp Ser Val	Val Leu Gly Ser Leu	Gln Arg Glu Gly Leu	
110	115	120	
Ser Pro Gly Ala Glu	Glu Val Gly Val Ala	Ala Leu Gln Leu Pro	
125	130	135	
Arg Ala Tyr Asn His	Tyr Ser Gln Gly Ser	Asp Leu Ala Leu Leu	
140	145	150	
Gln Leu Ala His Pro	Thr Thr His Thr Pro	Leu Cys Leu Pro Gln	
155	160	165	
Pro Ala His Arg Phe	Pro Phe Gly Ala Ser	Cys Trp Ala Thr Gly	
170	175	180	
Trp Asp Gln Asp Thr	Ser Asp Ala Pro Gly	Thr Leu Arg Asn Leu	
185	190	195	
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Arg Leu Arg Leu Ile	Ser Arg Pro Thr Cys	Asn Cys Ile Tyr Asn	
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Gln Leu His Gln Arg	His Leu Ser Asn Pro	Ala Arg Pro Gly Met	
215	220	225	
Leu Cys Gly Gly Pro	Gln Pro Gly Val Gln	Gly Pro Cys Gln Gly	
230	235	240	
Asp Ser Gly Gly Pro	Val Leu Cys Leu Glu	Pro Asp Gly His Trp	
245	250	255	
Val Gln Ala Gly Ile	Ile Ser Phe Ala Ser	Ser Cys Ala Gln Glu	
260	265	270	
Asp Ala Pro Val Leu	Leu Thr Asn Thr Ala	Ala His Ser Ser Trp	
275	280	285	
Leu Gln Ala Arg Val	Gln Gly Ala Ala Phe	Leu Ala Gln Ser Pro	
290	295	300	
Glu Thr Pro Glu Met	Ser Asp Glu Asp Ser	Cys Val Ala Cys Gly	
305	310	315	



Ser Leu Arg Thr Ala Gly Pro Gln Ala Gly Ala Pro Ser Pro Trp  
320 325 330

Pro Trp Glu Ala Arg Leu Met His Gln Gly Gln Leu Ala Cys Gly  
335 340 345

Gly Ala Leu Val Ser Glu Glu Ala Val Leu Thr Ala Ala His Cys  
350 355 360

Phe Ile Gly Arg Gln Ala Pro Glu Glu Trp Ser Val Gly Leu Gly  
365 370 375

Thr Arg Pro Glu Glu Trp Gly Leu Lys Gln Leu Ile Leu His Gly  
380 385 390

Ala Tyr Thr His Pro Glu Gly Gly Tyr Asp Met Ala Leu Leu Leu  
395 400 405

Leu Ala Gln Pro Val Thr Leu Gly Ala Ser Leu Arg Pro Leu Cys  
410 415 420

Leu Pro Tyr Pro Asp His His Leu Pro Asp Gly Glu Arg Gly Trp  
425 430 435

Val Leu Gly Arg Ala Arg Pro Gly Ala Gly Ile Ser Ser Leu Gln  
440 445 450

Thr Val Pro Val Thr Leu Leu Gly Pro Arg Ala Cys Ser Arg Leu  
455 460 465

His Ala Ala Pro Gly Gly Asp Gly Ser Pro Ile Leu Pro Gly Met  
470 475 480

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Val Cys Thr Ser Ala Val Gly Glu Leu Pro Ser Cys Glu Gly Leu  
485 490 495

Ser Gly Ala Pro Leu Val His Glu Val Arg Gly Thr Trp Phe Leu  
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Ala Gly Leu His Ser Phe Gly Asp Ala Cys Gln Gly Pro Ala Arg  
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Pro Ala Val Phe Thr Ala Leu Pro Ala Tyr Glu Asp Trp Val Ser  
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Cys

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<212> DNA

<213> Artificial Sequence

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

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			20						25					30

Val	Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp
			35						40					45

Ala	Thr	Leu	Cys	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu
			50						55					60

Ala	Gln	Leu	Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu
			65						70					75

Val	His	Ser	Phe	Ala	Glu	Gly	Gln	Asp	Gln	Gly	Ser	Ala	Tyr	Ala
			80						85					90

Asn	Arg	Thr	Ala	Leu	Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala
			95						100					105

Ser	Leu	Arg	Leu	Gln	Arg	Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe
			110						115					120

Thr	Cys	Phe	Val	Ser	Ile	Arg	Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser
			125						130					135

Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	Lys	Pro	Ser	Met	Thr	Leu	Glu
			140						145					150

Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys
			155						160					165

Ser	Ser	Tyr	Gln	Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp
			170						175					180

Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met
			185						190					195

Ala	Asn	Glu	Gln	Gly	Leu	Phe	Asp	Val	His	Ser	Val	Leu	Arg	Val
			200						205					210

Val	Leu	Gly	Ala	Asn	Gly	Thr	Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro
			215						220					225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	230	235	240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	245	250	255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	260	265	270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	275	280	285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	290	295	300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	305	310	315

Ala

<210> 138  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
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<210> 139  
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<220>  
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<400> 139  
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<210> 140  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24

<212> DNA  
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<220>  
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<400> 141  
tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
<211> 24  
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<223> Synthetic oligonucleotide probe

<400> 142  
tggaagaaga gggtagtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
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<223> Synthetic oligonucleotide probe

<400> 143  
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<210> 144  
<211> 2336

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
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aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcactccac tcacaaacat aacaatggc agccatttg 400

gtttaccctg ggcacacctg aggcctctcaa aggttgggac cagggcttga 450  
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 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30

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Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
				35					40					45
Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
				50					55					60
Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
				65					70					75
Trp	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
				80					85					90
Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Leu	Ile	Ile
				95					100					105
Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
				110					115					120
Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
				125					130					135
Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
				140					145					150



Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
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Leu

<210> 146  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 146  
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<210> 147  
 <211> 25  
 <212> DNA  
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 <223> Synthetic oligonucleotide probe

<400> 147  
 gccagagca ggaggaatga tgagc 25

<210> 148  
 <211> 49  
 <212> DNA  
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<220>  
 <223> Synthetic oligonucleotide probe

<400> 148  
 gtggaacgcg gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149  
 <211> 2196  
 <212> DNA  
 <213> Homo sapiens

<400> 149  
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cacccctctcc cgtagcccac ccgactaaca tctcagtctc tgaaaatgca 150  
cagagatgcc tggctacctc gccctgcctt cagcctcacg gggctcagtc 200  
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gccacccctca acgtcctcaa tggctctgac gcccgcctgc cctgcacctt 300  
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aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450  
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<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

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Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
			20						25					30

Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45

Ala	Arg	Leu	Pro	Cys	Thr	Phe	Asn	Ser	Cys	Tyr	Thr	Val	Asn	His
				50					55					60

Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75

Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80					85					90

Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105

Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu
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Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<210> 151  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

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 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
 gccctgcctt cagcctcaag gggctcagtc tctttttctc tttggtgcc 200  
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
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 caactgctac atcatgaacc cccc 524

<210> 152

<211> 368  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 56, 123  
<223> unknown base

<400> 152  
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ccctgaactg gatttaccag gagtgcaca actggctctg aggagatgtt 200  
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ctacatcatg aaccccc 368

<210> 153  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<400> 153  
acggagcatg gaggtccaca gtac 24

<210> 154  
<211> 23  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 154  
gcacgtttct cagcatcacc gac 23

<210> 155  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 155

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<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

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cggcaggaca cagaagggt ggtggaagcc acgatgccac ctggcgtgca 1000

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tgactggctt cctgggcgag cctagtagct cctgcaggca ggggcagttt 1850  
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cctcccttac caccaggagc attcaagctc tggattgggc agcagatgtg 1950  
ccccagtc cgcaggctgt gttccagggg ccctgatttc ctcggatgtg 2000  
ctattggccc caggactgaa gctgcctccc ttcacctgg gactgtggtt 2050

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ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100  
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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20					25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Glu	Glu	Met	Tyr	Gln	Leu	Tyr	Gly	Gly	Pro	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



	245		250		255
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260		265		270
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275		280		285
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290		295		300
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305		310		315
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320		325		330
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335		340		345
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350		355		360
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365		370		375
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380		385		390
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395		400		405

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 158  
 ctggggctac acacggggtg agg 23

<210> 159  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 159  
 ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
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<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
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gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tctgcacatc atggtgaggg ctacagcaat 200  
gcccacgagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcca tcgggggtgct ggccttcctg gcctcggcct 300  
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cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400  
cctgtggttt gttggtttct gcttcctcac caaccagtgg gcagtcacca 450  
accgaagga cgtgctggtg ggggccgact ctgtgagggc agccatcacc 500  
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gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700  
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 gtgccccatg gctccagac tctgtctgtg ccgagtgtat tataaaatcg 1450  
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 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe
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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val
				95					100					105

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu  
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn  
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr  
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln  
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr  
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaaggtga tggctgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ccacgagtct aagcagatgt actgctgtt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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ctggcgggca gggggacgga ggtgatggcg aggaagcgga gccagagggg 150

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tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca ccgcctggg aatttactac 450

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<210> 169

<211> 802

<212> PRT

<213> Homo sapiens

<400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp
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Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala
			20						25					30

Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val
				35					40					45

Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly
				50					55					60

Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val
				65					70					75

Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe
				80					85					90

Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu
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	95	100	105
Thr Ala Lys Ala	Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr	
	110	115	120
Arg Leu Gly Thr	Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly	
	125	130	135
Glu Gly Pro Leu	Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro	
	140	145	150
Glu His Arg Arg	Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu	
	155	160	165
Leu Val Glu Glu	Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val	
	170	175	180
Pro Tyr Arg Ala	Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile	
	185	190	195
Leu Glu Ala Ser	Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu	
	200	205	210
Gly Cys Tyr Arg	Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg	
	215	220	225
Leu Lys Gly Pro	Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu	
	230	235	240
Gln Gly Pro Lys	Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr	
	245	250	255
Leu Ala Glu Cys	Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly	
	260	265	270
Pro Leu Glu Lys	Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg	
	275	280	285
Gln Glu Pro Val	Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala	
	290	295	300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val	
	305	310	315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn Leu	
	320	325	330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro	
	335	340	345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His	
	350	355	360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe Asp	
	365	370	375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln	



380										385					390				
Gly	Gln	Trp	Thr	Ile	Gln	Asn	Arg	Arg	Leu	Cys	Gly	Leu	Arg	Ile					
				395					400					405					
Leu	Gln	Pro	Tyr	Ala	Glu	Arg	Ile	Pro	Val	Val	Ala	Thr	Ala	Gly					
				410					415					420					
Ile	Thr	Ile	Asn	Phe	Thr	Ser	Gln	Ile	Ser	Leu	Thr	Gly	Pro	Gly					
				425					430					435					
Val	Arg	Val	His	Tyr	Gly	Leu	Tyr	Asn	Gln	Ser	Asp	Pro	Cys	Pro					
				440					445					450					
Gly	Glu	Phe	Leu	Cys	Ser	Val	Asn	Gly	Leu	Cys	Val	Pro	Ala	Cys					
				455					460					465					
Asp	Gly	Val	Lys	Asp	Cys	Pro	Asn	Gly	Leu	Asp	Glu	Arg	Asn	Cys					
				470					475					480					
Val	Cys	Arg	Ala	Thr	Phe	Gln	Cys	Lys	Glu	Asp	Ser	Thr	Cys	Ile					
				485					490					495					
Ser	Leu	Pro	Lys	Val	Cys	Asp	Gly	Gln	Pro	Asp	Cys	Leu	Asn	Gly					
				500					505					510					
Ser	Asp	Glu	Glu	Gln	Cys	Gln	Glu	Gly	Val	Pro	Cys	Gly	Thr	Phe					
				515					520					525					
Thr	Phe	Gln	Cys	Glu	Asp	Arg	Ser	Cys	Val	Lys	Lys	Pro	Asn	Pro					
				530					535					540					
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His	Cys	Asp	Cys	Gly	Leu	Gln	Gly	Pro	Ser	Ser	Arg	Ile	Val	Gly					
				560					565					570					
Gly	Ala	Val	Ser	Ser	Glu	Gly	Glu	Trp	Pro	Trp	Gln	Ala	Ser	Leu					
				575					580					585					
Gln	Val	Arg	Gly	Arg	His	Ile	Cys	Gly	Gly	Ala	Leu	Ile	Ala	Asp					
				590					595					600					
Arg	Trp	Val	Ile	Thr	Ala	Ala	His	Cys	Phe	Gln	Glu	Asp	Ser	Met					
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Ala	Ser	Thr	Val	Leu	Trp	Thr	Val	Phe	Leu	Gly	Lys	Val	Trp	Gln					
				620					625					630					
Asn	Ser	Arg	Trp	Pro	Gly	Glu	Val	Ser	Phe	Lys	Val	Ser	Arg	Leu					
				635					640					645					
Leu	Leu	His	Pro	Tyr	His	Glu	Glu	Asp	Ser	His	Asp	Tyr	Asp	Val					
				650					655					660					
Ala	Leu	Leu	Gln	Leu	Asp	His	Pro	Val	Val	Arg	Ser	Ala	Ala	Val					

665	670	675
Arg Pro Val Cys	Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly	
680	685	690
Leu His Cys Trp	Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn	Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys	Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala	Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly	Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala	Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg	
770	775	780
Pro Asn Tyr Phe	Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser	
785	790	795
Trp Ile Gln Gln	Val Val Thr	
800		

<210> 170  
 <211> 1327  
 <212> DNA  
 <213> Homo\_sapiens

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 caccatcaac ttcacctccc agatctccct caccgggccc ggtgtgcggg 150  
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200  
 tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 cccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggctctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaaccgcga gtgtgatggg cggcccgaact gcagggacgg ctcggatgag 500  
 gagcactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550

agctgtgtcc tccgaggggtg agtggccatg gcaggccagc ctccagggtc 600  
 ggggtcgaca catctgtggg ggggccctca tcgctgaccg ctgggtgata 650  
 acagctgccc actgttcca ggaggacagc atggcctcca cggtgctgtg 700  
 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750  
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800  
 agccatgact acgacgtggc gctgctgcag ctcgaccacc cgggtgtgag 850  
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 ggacctgtgc agcgaggcct atcgctacca ggtgacgcca cgcattgtgt 1050  
 gtgcccgtta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150  
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200  
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300  
 gcaactgcca agcaggggga caagtat 1327

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<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcaggccg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

tgccctatgca ctgaggaggc agaag 25

<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

aggcagggac acagagtcca ttcac 25

<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50

ccaccgcccg ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100

ctccagtccc ccagcccctg gccgagagaa gggctcttacc ggccgggatt 150

gctggaaaca ccaagagggt gtttttgttt tttaaaactt ctgtttcttg 200

ggaggggggtg tggcggggca ggatgagcaa ctccgttccct ctgctctgtt 250

tctggagcct ctgctattgc tttgctgcgg ggagccccgt accttttggt 300  
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tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
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aaaaaaaaaa 1510

<210> 178  
<211> 354  
<212> PRT  
<213> Homo sapiens

<400> 178

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr  
1 5 10 15

Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg  
20 25 30

Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val  
35 40 45

Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu  
50 55 60

His Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu  
65 70 75

Asp Cys Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His  
80 85 90

Gly Trp Thr Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu  
95 100 105

Val Ser Ala Leu His Thr Arg Glu Lys Asp Ala Asn Val Val Val  
110 115 120

Val Asp Trp Leu Pro Leu Ala His Gln Leu Tyr Thr Asp Ala Val  
125 130 135

Asn Asn Thr Arg Val Val Gly His Ser Ile Ala Arg Met Leu Asp  
140 145 150

Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu Gly Asn Val His Leu  
155 160 165

Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly Tyr Ala Gly Asn  
170 175 180

Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu Asp Pro Ala  
185 190 195

Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu Ser Pro  
200 205 210

Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg Ser  
215 220 225

Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp  
230 235 240

Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn  
245 250 255

Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val  
260 265 270

Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu  
275 280 285

Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser  
290 295 300

Asn Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg  
305 310 315

Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg  
320 325 330

Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg  
335 340 345

Gly Asn Leu Gln Ser Leu Glu Cys Pro  
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

gtgagcatga gcgagccgtc cac 23

<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

ttgactctct ggtgaatcag gacaagccga gttttgcott ccag 44

<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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acgcgctgga ggagtggagc agcaccggc cgccctggg ggctgacagt 150  
cggcaaagtt tggcccgaag aggaagtggc ctcaaacc cggcaggtggc 200  
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<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

Met	Leu	Leu	Ala	Thr	Leu	Leu	Leu	Leu	Leu	Gly	Gly	Ala	Leu	1	5	10	15
Ala	His	Pro	Asp	Arg	Ile	Ile	Phe	Pro	Asn	His	Ala	Cys	Glu	Asp	20	25	30
Pro	Pro	Ala	Val	Leu	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165
Gly	Asp	Gly	Ser	Asp	Glu	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr			

	185		190		195
Leu Glu Asp Phe	Tyr Gly Val Phe Ser	Ser Pro Gly Tyr Thr	His		
	200	205	210		
Leu Ala Ser Val	Ser His Pro Gln Ser	Cys His Trp Leu Leu	Asp		
	215	220	225		
Pro His Asp Gly	Arg Arg Leu Ala Val	Arg Phe Thr Ala Leu	Asp		
	230	235	240		
Leu Gly Phe Gly	Asp Ala Val His Val	Tyr Asp Gly Pro Gly	Pro		
	245	250	255		
Pro Glu Ser Ser	Arg Leu Leu Arg Ser	Leu Thr His Phe Ser	Asn		
	260	265	270		
Gly Lys Ala Val	Thr Val Glu Thr Leu	Ser Gly Gln Ala Val	Val		
	275	280	285		
Ser Tyr His Thr	Val Ala Trp Ser Asn	Gly Arg Gly Phe Asn	Ala		
	290	295	300		
Thr Tyr His Val	Arg Gly Tyr Cys Leu	Pro Trp Asp Arg Pro	Cys		
	305	310	315		
Gly Leu Gly Ser	Gly Leu Gly Ala Gly	Glu Gly Leu Gly Glu	Arg		
	320	325	330		
Cys Tyr Ser Glu	Ala Gln Arg Cys Asp	Gly Ser Trp Asp Cys	Ala		
	335	340	345		
Asp Gly Thr Asp	Glu Glu Asp Cys Pro	Gly Cys Pro Pro Gly	His		
	350	355	360		
Phe Pro Cys Gly	Ala Ala Gly Thr Ser	Gly Ala Thr Ala Cys	Tyr		
	365	370	375		
Leu Pro Ala Asp	Arg Cys Asn Tyr Gln	Thr Phe Cys Ala Asp	Gly		
	380	385	390		
Ala Asp Glu Arg	Arg Cys Arg His Cys	Gln Pro Gly Asn Phe	Arg		
	395	400	405		
Cys Arg Asp Glu	Lys Cys Val Tyr Glu	Thr Trp Val Cys Asp	Gly		
	410	415	420		
Gln Pro Asp Cys	Ala Asp Gly Ser Asp	Glu Trp Asp Cys Ser	Tyr		
	425	430	435		
Val Leu Pro Arg	Lys Val Ile Thr Ala	Ala Val Ile Gly Ser	Leu		
	440	445	450		
Val Cys Gly Leu	Leu Leu Val Ile Ala	Leu Gly Cys Thr Cys	Lys		
	455	460	465		
Leu Tyr Ala Ile	Arg Thr Gln Glu Tyr	Ser Ile Phe Ala Pro	Leu		

470	475	480
Ser Arg Met Glu	Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser	
485	490	495
Tyr Gly Gln Leu	Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp	
500	505	510
Phe Pro Thr Glu	Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu	
515	520	525
Arg Ser Leu Leu	Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly	
530	535	540
Gly Pro Gly Ala	Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg	
545	550	555
Leu Val Arg Arg	Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn	
560	565	570
Thr Pro Ala Arg	Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser	
575	580	585
Ala Ala Pro Leu	Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg	
590	595	600
Glu Gly Gly Ala	Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro	
605	610	615
Leu Pro Ile Lys	Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala	
620	625	630
Pro Thr Thr Val	Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro	
635	640	645
Leu Glu Pro Ser	Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly	
650	655	660
Arg Leu Leu Pro	Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro	
665	670	675
Pro Gly Pro His	Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp	
680	685	690
Val Leu Leu Val	Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu	
695	700	705
Ala Glu Asp Glu	Pro Leu Leu Thr	
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaaggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<400> 187  
tgcttgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttgga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
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gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150  
 aataaaacat cgcccccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
 tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
 gcccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350  
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
 atgctcatcg tatctgtgtt ggcactgata ccagaaacca caacattgac 450  
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 acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600  
 tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
 aaaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
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Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
				20					25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
				35					40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
				50					55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
				65					70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
				80					85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
				95					100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
				110					115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
				125					130					135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu  
140 145 150

Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
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ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catcgcccct tctgttcag tgtgaaaggc cacgtgaaga tgctgcggt 200  
ggcactaact gngacatcta tgacctttt tatnatcgca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcacogttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggt aacaacagta ttcattgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggacg 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccgcg cgccggccga gtcgctgagc cgcggctgcc ggacgggacg 50

ggaccggcta ggctgggagc gccccccggg ccccgccgtg ggcatgggag 100

caactggcccg ggcgctgctg ctgcctctgc tggcccagtg gctcctgagc 150

gccgccccgg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200

cgcggccacg aaccgcgtag ttgcgccac cccgggaccc gggacccttg 250

ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgcctggcg 300

tcccccgagg ggcgcgcca cttcttgccc atggtagaca acctgcaggg 350

ggactctggc cgcggctact acctggagat gctgatcggg accccccgc 400

agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450

ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500

cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550

gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600

aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650

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acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800

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gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950



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aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT.

<213> Homo sapien

<400> 196

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Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
			20						25					30

Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45

Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225

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Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Glu	Tyr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr	Asn	Ser	Glu	Thr	Pro	Trp	Ser	Tyr	Phe	Pro	Lys	Ile	Ser	Ile	350	355	360
Tyr	Leu	Arg	Asp	Glu	Asn	Ser	Ser	Arg	Ser	Phe	Arg	Ile	Thr	Ile	365	370	375
Leu	Pro	Gln	Leu	Tyr	Ile	Gln	Pro	Met	Met	Gly	Ala	Gly	Leu	Asn	380	385	390
Tyr	Glu	Cys	Tyr	Arg	Phe	Gly	Ile	Ser	Pro	Ser	Thr	Asn	Ala	Leu	395	400	405
Val	Ile	Gly	Ala	Thr	Val	Met	Glu	Gly	Phe	Tyr	Val	Ile	Phe	Asp	410	415	420
Arg	Ala	Gln	Lys	Arg	Val	Gly	Phe	Ala	Ala	Ser	Pro	Cys	Ala	Glu	425	430	435
Ile	Ala	Gly	Ala	Ala	Val	Ser	Glu	Ile	Ser	Gly	Pro	Phe	Ser	Thr	440	445	450
Glu	Asp	Val	Ala	Ser	Asn	Cys	Val	Pro	Ala	Gln	Ser	Leu	Ser	Glu	455	460	465
Pro	Ile	Leu	Trp	Ile	Val	Ser	Tyr	Ala	Leu	Met	Ser	Val	Cys	Gly	470	475	480
Ala	Ile	Leu	Leu	Val	Leu	Ile	Val	Leu	Leu	Leu	Pro	Phe	Arg		485	490	495
Cys	Gln	Arg	Arg	Pro	Arg	Asp	Pro	Glu	Val	Val	Asn	Asp	Glu	Ser	500	505	510

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Ser Leu Val Arg His Arg Trp Lys  
515

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 197

cgcagaagct acagattctc g 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 198

ggaaattgga ggccaaagc 19

<210> 199  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 199  
ggatgtagcc agcaactgtg 20

<210> 200  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 200  
gccttggtc gttctcttc 19

<210> 201  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 201  
ggtcctgtgc ctggatgg 18

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<210> 202  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 202  
gacaagacta cctccgttgg tc 22

<210> 203  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 203  
tgatgcacag ttcagcacct gttg 24

<210> 204

<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 204  
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
<211> 1939  
<212> DNA  
<213> Homo sapiens

<400> 205  
cgctccgcc ttcgagggt gacgcgccg ggcgccgttc caggcctgtg 50  
cagggcggtat cggcagccgc ctggcgccga tccagggcgg tgcggggcct 100  
gggcgggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
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ttccgggagg atgcagggtt ggggtcatct gtatctgaag cccctcgaa 1900

taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met	Glu	Ala	Leu	Leu	Leu	Gly	Ala	Gly	Leu	Leu	Leu	Gly	Ala	Tyr
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Val	Leu	Val	Tyr	Tyr	Asn	Leu	Val	Lys	Ala	Pro	Pro	Cys	Gly	Gly
				20					25					30

Met	Gly	Asn	Leu	Arg	Gly	Arg	Thr	Ala	Val	Val	Thr	Gly	Ala	Asn
				35					40					45

Ser	Gly	Ile	Gly	Lys	Met	Thr	Ala	Leu	Glu	Leu	Ala	Arg	Arg	Gly
				50					55					60

Ala	Arg	Val	Val	Leu	Ala	Cys	Arg	Ser	Gln	Glu	Arg	Gly	Glu	Ala
				65					70					75

Ala	Ala	Phe	Asp	Leu	Arg	Gln	Glu	Ser	Gly	Asn	Asn	Glu	Val	Ile	80	85	90
Phe	Met	Ala	Leu	Asp	Leu	Ala	Ser	Leu	Ala	Ser	Val	Arg	Ala	Phe	95	100	105
Ala	Thr	Ala	Phe	Leu	Ser	Ser	Glu	Pro	Arg	Leu	Asp	Ile	Leu	Ile	110	115	120
His	Asn	Ala	Gly	Ile	Ser	Ser	Cys	Gly	Arg	Thr	Arg	Glu	Ala	Phe	125	130	135
Asn	Leu	Leu	Leu	Arg	Val	Asn	His	Ile	Gly	Pro	Phe	Leu	Leu	Thr	140	145	150
His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln  
365 370 375

Leu Ser

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<223> Synthetic oligonucleotide probe

<400> 207  
cttcatggcc ttggacttgg ccag 24

<210> 208  
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<212> DNA  
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<220>  
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<400> 208  
acgccagtgg cctcaagctg gttg 24

<210> 209  
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<400> 209  
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<210> 210  
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<212> DNA  
<213> Homo sapiens

<400> 210  
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acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150  
caagcctcag gccagccacc tcccaccatc cgctggttgc tgaatgggca 200  
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aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgga 2400  
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cagagttcac ggacatgggc aggactggag gaggggtggg gcccagggg 2550

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ggagtcttgc tgtgccacc tcggccctgc ctaccccca ccccagcga 2600  
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<210> 211  
 <211> 985  
 <212> PRT  
 <213> Homo sapiens

<400> 211

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Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
				20					25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys Gly Pro Pro Trp Gly His Pro Glu Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys Pro Leu Ala Leu Gln Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser Leu Leu Met Ala Arg Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met Cys Val Ala Thr Asn Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala Arg Val Ser Ile Gln Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu Leu Leu Ala Val Arg Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn Pro Asp Pro Ala Glu Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu Ser Trp Lys Val Ser Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr Ala Leu Phe Arg Thr Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro Trp Ala Glu Glu Leu Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly Gly Leu His Trp Gly Gln Asp Tyr Glu Phe Lys	290	295	300
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Val Arg Pro Ser Ser Gly Arg Ala Arg Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg Leu Pro Glu Lys Val Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu Lys Pro Gly Asn Gly Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro Ala Glu Asn His Asn Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser Leu Gly Asn Thr Ser Leu Pro Pro Ala Asn Trp	365	370	375
Thr Val Val Gly Glu Gln Thr Gln Leu Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr Cys Val Gln Val Ala Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro Ser Arg Pro Val Cys Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser Glu His Gly Pro Trp Thr  
425 430 435

Leu Glu Gln Leu Arg Ala Thr Leu Lys Arg Pro Glu Val Ile Ala  
440 445 450

Thr Cys Gly Val Ala Leu Trp Leu Leu Leu Leu Gly Thr Ala Val  
455 460 465

Cys Ile His Arg Arg Arg Arg Ala Arg Val His Leu Gly Pro Gly  
470 475 480

Leu Tyr Arg Tyr Thr Ser Glu Asp Ala Ile Leu Lys His Arg Met  
485 490 495

Asp His Ser Asp Ser Gln Trp Leu Ala Asp Thr Trp Arg Ser Thr  
500 505 510

Ser Gly Ser Arg Asp Leu Ser Ser Ser Ser Ser Leu Ser Ser Arg  
515 520 525

Leu Gly Ala Asp Ala Arg Asp Pro Leu Asp Cys Arg Arg Ser Leu  
530 535 540

Leu Ser Trp Asp Ser Arg Ser Pro Gly Val Pro Leu Leu Pro Asp  
545 550 555

Thr Ser Thr Phe Tyr Gly Ser Leu Ile Ala Glu Leu Pro Ser Ser  
560 565 570

Thr Pro Ala Arg Pro Ser Pro Gln Val Pro Ala Val Arg Arg Leu  
575 580 585

Pro Pro Gln Leu Ala Gln Leu Ser Ser Pro Cys Ser Ser Ser Asp  
590 595 600

Ser Leu Cys Ser Arg Arg Gly Leu Ser Ser Pro Arg Leu Ser Leu  
605 610 615

Ala Pro Ala Glu Ala Trp Lys Ala Lys Lys Lys Gln Glu Leu Gln  
620 625 630

His Ala Asn Ser Ser Pro Leu Leu Arg Gly Ser His Ser Leu Glu  
635 640 645

Leu Arg Ala Cys Glu Leu Gly Asn Arg Gly Ser Lys Asn Leu Ser  
650 655 660

Gln Ser Pro Gly Ala Val Pro Gln Ala Leu Val Ala Trp Arg Ala  
665 670 675

Leu Gly Pro Lys Leu Leu Ser Ser Ser Asn Glu Leu Val Thr Arg  
680 685 690

His Leu Pro Pro Ala Pro Leu Phe Pro His Glu Thr Pro Pro Thr  
695 700 705

Gln	Ser	Gln	Gln	Thr	Gln	Pro	Pro	Val	Ala	Pro	Gln	Ala	Pro	Ser	
				710					715					720	
Ser	Ile	Leu	Leu	Pro	Ala	Ala	Pro	Ile	Pro	Ile	Leu	Ser	Pro	Cys	
				725					730					735	
Ser	Pro	Pro	Ser	Pro	Gln	Ala	Ser	Ser	Leu	Ser	Gly	Pro	Ser	Pro	
				740					745					750	
Ala	Ser	Ser	Arg	Leu	Ser	Ser	Ser	Ser	Leu	Ser	Ser	Leu	Gly	Glu	
				755					760					765	
Asp	Gln	Asp	Ser	Val	Leu	Thr	Pro	Glu	Glu	Val	Ala	Leu	Cys	Leu	
				770					775					780	
Glu	Leu	Ser	Glu	Gly	Glu	Glu	Thr	Pro	Arg	Asn	Ser	Val	Ser	Pro	
				785					790					795	
Met	Pro	Arg	Ala	Pro	Ser	Pro	Pro	Thr	Thr	Tyr	Gly	Tyr	Ile	Ser	
				800					805					810	
Val	Pro	Thr	Ala	Ser	Glu	Phe	Thr	Asp	Met	Gly	Arg	Thr	Gly	Gly	
				815					820					825	
Gly	Val	Gly	Pro	Lys	Gly	Gly	Val	Leu	Leu	Cys	Pro	Pro	Arg	Pro	
				830					835					840	
Cys	Leu	Thr	Pro	Thr	Pro	Ser	Glu	Gly	Ser	Leu	Ala	Asn	Gly	Trp	
				845					850					855	
Gly	Ser	Ala	Ser	Glu	Asp	Asn	Ala	Ala	Ser	Ala	Arg	Ala	Ser	Leu	
				860					865					870	
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Val	Ser	Ser	Ser	Asp	Gly	Ser	Phe	Leu	Ala	Asp	Ala	His	Phe	Ala	
				875					880					885	
Arg	Ala	Leu	Ala	Val	Ala	Val	Asp	Ser	Phe	Gly	Phe	Gly	Leu	Glu	
				890					895					900	
Pro	Arg	Glu	Ala	Asp	Cys	Val	Phe	Ile	Asp	Ala	Ser	Ser	Pro	Pro	
				905					910					915	
Ser	Pro	Arg	Asp	Glu	Ile	Phe	Leu	Thr	Pro	Asn	Leu	Ser	Leu	Pro	
				920					925					930	
Leu	Trp	Glu	Trp	Arg	Pro	Asp	Trp	Leu	Glu	Asp	Met	Glu	Val	Ser	
				935					940					945	
His	Thr	Gln	Arg	Leu	Gly	Arg	Gly	Met	Pro	Pro	Trp	Pro	Pro	Asp	
				950					955					960	
Ser	Gln	Ile	Ser	Ser	Gln	Arg	Ser	Gln	Leu	His	Cys	Arg	Met	Pro	
				965					970					975	
Lys	Ala	Gly	Ala	Ser	Pro	Val	Asp	Tyr	Ser						
				980					985						

<210> 212  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 212  
gaagggacct acatgtgtgt ggcc 24

<210> 213  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 213  
actgaccttc cagctgagcc acac 24

<210> 214  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 214  
aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

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<210> 215  
<211> 2749  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1869, 1887  
<223> unknown base

<400> 215  
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gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150  
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200  
tcgctgctct ggaccatct atgcagaaga agaaggccag gagacaatga 250  
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accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350  
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acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccagg 500  
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 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216  
 <211> 332  
 <212> PRT  
 <213> Homo sapiens

<400> 216  
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 20 25 30  
 Asp Thr Val Ser Leu Gln Cys Thr Tyr Arg Glu Glu Leu Arg Asp  
 35 40 45  
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg

	50		55		60
Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met	65		70		75
Lys Gly Arg Val Ser Ile Arg Asp Ser Arg Gln Glu Leu Ser Leu	80		85		90
Ile Val Thr Leu Trp Asn Leu Thr Leu Gln Asp Ala Gly Glu Tyr	95		100		105
Trp Cys Gly Val Glu Lys Arg Gly Pro Asp Glu Ser Leu Leu Ile	110		115		120
Ser Leu Phe Val Phe Pro Gly Pro Cys Cys Pro Pro Ser Pro Ser	125		130		135
Pro Thr Phe Gln Pro Leu Ala Thr Thr Arg Leu Gln Pro Lys Ala	140		145		150
Lys Ala Gln Gln Thr Gln Pro Pro Gly Leu Thr Ser Pro Gly Leu	155		160		165
Tyr Pro Ala Ala Thr Thr Ala Lys Gln Gly Lys Thr Gly Ala Glu	170		175		180
Ala Pro Pro Leu Pro Gly Thr Ser Gln Tyr Gly His Glu Arg Thr	185		190		195
Ser Gln Tyr Thr Gly Thr Ser Pro His Pro Ala Thr Ser Pro Pro	200		205		210
Ala Gly Ser Ser Arg Pro Pro Met Gln Leu Asp Ser Thr Ser Ala	215		220		225
Glu Asp Thr Ser Pro Ala Leu Ser Ser Gly Ser Ser Lys Pro Arg	230		235		240
Val Ser Ile Pro Met Val Arg Ile Leu Ala Pro Val Leu Val Leu	245		250		255
Leu Ser Leu Leu Ser Ala Ala Gly Leu Ile Ala Phe Cys Ser His	260		265		270
Leu Leu Leu Trp Arg Lys Glu Ala Gln Gln Ala Thr Glu Thr Gln	275		280		285
Arg Asn Glu Lys Phe Trp Leu Ser Arg Leu Thr Ala Glu Glu Lys	290		295		300
Glu Ala Pro Ser Gln Ala Pro Glu Gly Asp Val Ile Ser Met Pro	305		310		315
Pro Leu His Thr Ser Glu Glu Glu Leu Gly Phe Ser Lys Phe Val	320		325		330

Ser Ala

<210> 217  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 217  
ccctgcagtg cacctacagg gaag 24

<210> 218  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 218  
ctgtcttccc ctgcttggt gtgg 24

<210> 219  
<211> 47  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 219  
ggtgcaggaa ggggtgggatac ctcttctctc gctgctctgg ccacatc 47

<210> 220  
<211> 950  
<212> DNA  
<213> Homo sapiens

<400> 220  
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gggggtggcag gagccgcaga gccagagcag acagccgaga aacaggtgga 100  
cagtgtgaaa gaaccagtgg tctcgtctctg ttgccaggc tagagtgtac 150  
tggcgtgata atagctcaact gcagcctcag actcctggac ttgagaaatc 200  
ctcctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
cctgtttctt ctccttctgt gagtggacca cggaggctgg tgagctgcct 300  
gtcatcccaa agctcagctc tgagccagag tgggtggtggc tccacctctg 350  
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 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
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 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
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<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Asn	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 222  
gggatcatgt tgttggccct ggtc 24

<210> 223  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 223  
gcaaggcaga cccagtcagc cag 23

<210> 224  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 224  
ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

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<210> 225  
<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
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gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaagctgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcaggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctcggtgcgc gcggtgccc 250  
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tgctccacac tcgactcctt gcccgctcttc ggcaagggtg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400  
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gacaggacag tgcattgggt cagccacag ggcttcaggt ggtaaggatg 500  
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ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga ggggcccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgaggctt ccacacggcg cagggtggagc 1000  
tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggtttggt ttttgggtcc tcatgttatt tattgcgaa accaggcagg 1250

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caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350  
gtgccactg accactcagt tgttatctgt gtccgttttt ctacttgacg 1400  
acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
atggaagtca caccctctgg aaaaaagaac tottaactct ccagcacaca 1550  
tacacatgga ctctggcag cttgagccta gaagccatgt ctctcaaag 1600  
ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
tcagccctta catggacagc tagaggttcg atatctgtgg gtccttcag 1700  
gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
cccagcctgc cccagcctgc ccctgggaag aggaaactta accactcccc 1800  
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850

gctgtgcctt tgcagtcacg cccgagtcac ctttcacagc gctgttcctc 1900  
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
acacacacac ggacacacac acacacctgc gagagagagg gaggaaaggg 2000  
ctgtgccttt gcagtcacgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
<211> 351  
<212> PRT  
<213> Homo sapiens

<400> 226

Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
1 5 10 15

Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
20 25 30

Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
35 40 45

Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
50 55 60

Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
65 70 75

Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
80 85 90

Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
95 100 105

Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
110 115 120

Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys  
125 130 135

Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe  
140 145 150

Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe  
155 160 165

Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser  
170 175 180

Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg  
185 190 195

Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly  
200 205 210

Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro

	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtgggaga ctgtttaaat tatcggcc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>



<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctcgtggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50

gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcggca 100

gctccgagga ggtccccgga gggccctggg gacgctgggt gacttggagc 150

aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcctttg 200

ggctgtgatt ctgagtatcc tattgtccaa ggcctccacg gagcgcgcgg 250

cgtgcttga cggccacgac ctgctgagga caaacgcctc gaagcagacg 300

gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350

ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400

cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450

cgcgtgaccc agggcttggc tgaagccggc agggggcgtg aggacgtccg 500

cactgagctg ttccggggcg tggaggccgt gaggtccag aacaactcct 550

gcgagccgtg cccacgctcg tggctgtcct tcgagggtc ctgctacttt 600

ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650

tgccagcgcg cacctggtga tcgttggggg cctggatgag cagggttcc 700

tcactcgga cacgcgtggc cgtggttact ggctgggcct gagggctgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800

cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850

agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900

gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950

ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000

gctgtcacc tccctggctc ctggagctga ttgccaaaga gttttttct 1050

tcctcatcca ccgctgctga gtctcagaaa cacttgccc aacatagccc 1100

tgtccagccc agtgccctgg ctctgggacc tccatgccga cctcatccta 1150

actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
ctcctgcgtc cccgtgatat gcctccactt ctctccctaa ccaagggttag 1250  
gtgactgagg actggagctg tttgggttttc tcgcattttc caccaaactg 1300  
gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
1 5 10 15

Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
20 25 30

Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
35 40 45

Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
50 55 60

Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
65 70 75

Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
80 85 90

Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
95 100 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
110 115 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
125 130 135

Glu Ala Gly Arg Gly Arg Glu Asp Val Arg Thr Glu Leu Phe Arg  
140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys  
155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser  
170 175 180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp  
185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly  
200 205 210

Phe Leu Thr Arg Asn Thr Arg Gly Arg Gly Tyr Trp Leu Gly Leu  
215 220 225

Arg Ala Val Arg His Leu Gly Lys Val Gln Gly Tyr Gln Trp Val  
230 235 240

Asp Gly Val Ser Leu Ser Phe Ser His Trp Asn Gln Gly Glu Pro  
245 250 255

Asn Asp Ala Trp Gly Arg Glu Asn Cys Val Met Met Leu His Thr  
260 265 270

Gly Leu Trp Asn Asp Ala Pro Cys Asp Ser Glu Lys Asp Gly Trp  
275 280 285

Ile Cys Glu Lys Arg His Asn Cys  
290

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gaggggtgatc cgacccgggg aaggtcgctg ggcagggcga 50

gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100

ctcccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150

agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200

gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250

cgctcccgt gctcctgccg ggtgatggaa aaccccagcc cggccgccgc 300

cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350

gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400

tacagcatca ccttcacggg caagtggagc cagacggcct tccccaagca 450

gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500

cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550

gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600

gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650

cgcccgcct cccagcggc accgggcaga cgtcggcgga gctggagggtg 700

cagcgcaggc actcgctggg ctcgtttggt gtgcgcacgtg tgcccagccc 750

cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800

ggcgggaaca ggcggcgctg gacctgtacc cctacgacgc cgggacggac 850

agcggcttca cttctcctc ccccaacttc gccaccatcc cgcaggacac 900

ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950

actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000

cggctgcgac agagccccag ggccttcac cctcccgcc cagtccctgcc 1050

cagcagggac aatgagattg tagacagcgc ctacgttcca gaaacgccgc 1100

tggactgcga ggtctccctg tggtcgtcct ggggactgtg cggaggccac 1150

tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc gggtcagacc 1200

cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250

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cggagccatg ggggtgcggg ggctcctgtg caggctcatg ctgcaggcgg 1350

ccgagggcac aggggggttc gcgctgctcc tgaccgcggt gaggccgcgc 1400

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 gtctgtcttc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
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 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys  
 1 5 10 15

Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly  
 20 25 30

Gly Glu Ser Ile Cys Ser Ala Arg Ala Pro Ala Lys Tyr Ser Ile  
 35 40 45

Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr  
 50 55 60

Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala  
 65 70 75

Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val  
 80 85 90

Ser Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala  
 95 100 105

Leu Met Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val  
 110 115 120

His Glu Val Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln  
 125 130 135

Thr Ser Ala Glu Leu Glu Val Gln Arg Arg His Ser Leu Val Ser  
 140 145 150

Phe Val Val Arg Ile Val Pro Ser Pro Asp Trp Phe Val Gly Val  
 155 160 165

Asp	Ser	Leu	Asp	Leu	Cys	Asp	Gly	Asp	Arg	Trp	Arg	Glu	Gln	Ala	
				170					175					180	
Ala	Leu	Asp	Leu	Tyr	Pro	Tyr	Asp	Ala	Gly	Thr	Asp	Ser	Gly	Phe	
				185					190					195	
Thr	Phe	Ser	Ser	Pro	Asn	Phe	Ala	Thr	Ile	Pro	Gln	Asp	Thr	Val	
				200					205					210	
Thr	Glu	Ile	Thr	Ser	Ser	Ser	Pro	Ser	His	Pro	Ala	Asn	Ser	Phe	
				215					220					225	
Tyr	Tyr	Pro	Arg	Leu	Lys	Ala	Leu	Pro	Pro	Ile	Ala	Arg	Val	Thr	
				230					235					240	
Leu	Leu	Arg	Leu	Arg	Gln	Ser	Pro	Arg	Ala	Phe	Ile	Pro	Pro	Ala	
				245					250					255	
Pro	Val	Leu	Pro	Ser	Arg	Asp	Asn	Glu	Ile	Val	Asp	Ser	Ala	Ser	
				260					265					270	
Val	Pro	Glu	Thr	Pro	Leu	Asp	Cys	Glu	Val	Ser	Leu	Trp	Ser	Ser	
				275					280					285	
Trp	Gly	Leu	Cys	Gly	Gly	His	Cys	Gly	Arg	Leu	Gly	Thr	Lys	Ser	
				290					295					300	
Arg	Thr	Arg	Tyr	Val	Arg	Val	Gln	Pro	Ala	Asn	Asn	Gly	Ser	Pro	
				305					310					315	
Cys	Pro	Glu	Leu	Glu	Glu	Glu	Ala	Glu	Cys	Val	Pro	Asp	Asn	Cys	
				320					325					330	

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

caggactcgc tacgtccg 18

<210> 239  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 239  
cagcccccttc tcctcctttc tccc 24

<210> 240  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 240  
gcagttatca gggacgcact cagcc 25

<210> 241  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 241  
ccagcgagag gcagatag 18

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<210> 242  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 242  
cggtcaccgt gtcctgcggg atg 23

<210> 243  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 243  
cagcccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894  
<212> DNA  
<213> Homo sapiens

<400> 244

ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50  
tgtcttgctg gatattgaca aactgaagct ttcttgacc actggactta 100  
aggaagagtg tactcgtagg cggacagctt tagtgcccg cggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300  
cagaaatfff atccaactff gtttgaagc ttattatgac aataccatff 350  
ttcatagagt tgtgcctggg ttcatagtcc aaggcggaga tcctactggc 400  
acagggagtg gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtttta atcggagagg actggttgcc atggcaaattg 500  
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatcttt ggaaaggta caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
gaccacataa tccacacaaa ataaaaagct gtgaggtttt gtttaatcct 700  
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750  
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800  
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850  
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900  
ggatgatcca catctcagtt ctgttccagt tgtagaaagt gaaaaagggtg 950  
atgcaccaga tttagttgat gatggagaag atgaaagtgc agagcatgat 1000  
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050  
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100  
aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250  
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300



aggaagcaac agtcaaagaa gggaacttcc cggaagatc agacccttgc 1350  
 actgctgaac cagtttaaat ctaaactcac tcaagcaatt gctgaaacac 1400  
 ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450  
 tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500  
 catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
 ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
 agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650  
 acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
 gaaaagaagt atttttgaac ctgttgtctg gttttgaaaa acaattatct 1750  
 tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggtg 1800  
 catgtgtttt ttctagctg accttttata ttgctaaatc tgaaataaaa 1850  
 taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245

<211> 472

<212> PRT

<213> Homo sapiens

<400> 245

Met	Ser	Asn	Ile	Tyr	Ile	Gln	Glu	Pro	Pro	Thr	Asn	Gly	Lys	Val	1	5	10	15
Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser	20	25	30	
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu	35	40	45	
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly	50	55	60	
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Thr	Gly	Ser	Gly	Gly	65	70	75	
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg	80	85	90	
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly	95	100	105	
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	110	115	120	
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	125	130	135	

Asp Thr Val Tyr	Asn Met Leu Arg Leu	Ser Glu Val Asp Ile	Asp
	140	145	150
Asp Asp Glu Arg	Pro His Asn Pro His	Lys Ile Lys Ser Cys	Glu
	155	160	165
Val Leu Phe Asn	Pro Phe Asp Asp Ile	Ile Pro Arg Glu Ile	Lys
	170	175	180
Arg Leu Lys Lys	Glu Lys Pro Glu Glu	Glu Val Lys Lys Leu	Lys
	185	190	195
Pro Lys Gly Thr	Lys Asn Phe Ser Leu	Leu Ser Phe Gly Glu	Glu
	200	205	210
Ala Glu Glu Glu	Glu Glu Glu Val Asn	Arg Val Ser Gln Ser	Met
	215	220	225
Lys Gly Lys Ser	Lys Ser Ser His Asp	Leu Leu Lys Asp Asp	Pro
	230	235	240
His Leu Ser Ser	Val Pro Val Val Glu	Ser Glu Lys Gly Asp	Ala
	245	250	255
Pro Asp Leu Val	Asp Asp Gly Glu Asp	Glu Ser Ala Glu His	Asp
	260	265	270
Glu Tyr Ile Asp	Gly Asp Glu Lys Asn	Leu Met Arg Glu Arg	Ile
	275	280	285
Ala Lys Lys Leu	Lys Lys Asp Thr Ser	Ala Asn Val Lys Ser	Ala
	290	295	300
<hr/>			
Gly Glu Gly Glu	Val Glu Lys Lys Ser	Val Ser Arg Ser Glu	Glu
	305	310	315
Leu Arg Lys Glu	Ala Arg Gln Leu Lys	Arg Glu Leu Leu Ala	Ala
	320	325	330
Lys Gln Lys Lys	Val Glu Asn Ala Ala	Lys Gln Ala Glu Lys	Arg
	335	340	345
Ser Glu Glu Glu	Glu Ala Pro Pro Asp	Gly Ala Val Ala Glu	Tyr
	350	355	360
Arg Arg Glu Lys	Gln Lys Tyr Glu Ala	Leu Arg Lys Gln Gln	Ser
	365	370	375
Lys Lys Gly Thr	Ser Arg Glu Asp Gln	Thr Leu Ala Leu Leu	Asn
	380	385	390
Gln Phe Lys Ser	Lys Leu Thr Gln Ala	Ile Ala Glu Thr Pro	Glu
	395	400	405
Asn Asp Ile Pro	Glu Thr Glu Val Glu	Asp Asp Glu Gly Trp	Met
	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp  
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg  
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met  
455 460 465

Arg Glu Lys Lys Glu Arg Arg  
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

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caactggaac aggaactgag atgtggatc 29

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<213> Homo sapiens

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<212> PRT  
<213> Homo sapiens

<400> 254

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Thr	Val	Ala	Ala	Gly	Gly	Thr	Ser	Thr	Gly	Gly	Val	Phe	Ser	Phe
				20					25					30

Gly	Thr	Gly	Thr	Ser	Ser	Asn	Pro	Ser	Val	Gly	Leu	Asn	Phe	Gly
				35					40					45

Asn	Leu	Gly	Ser	Thr	Ser	Thr	Pro	Ala	Thr	Thr	Ser	Ala	Pro	Ser
				50					55					60

Ser	Gly	Phe	Gly	Thr	Gly	Leu	Phe	Gly	Ser	Lys	Pro	Ala	Thr	Gly
				65					70					75

Phe	Thr	Leu	Gly	Gly	Thr	Asn	Thr	Gly	Ala	Leu	His	Thr	Lys	Arg
				80					85					90

Pro	Gln	Val	Val	Thr	Lys	Tyr	Gly	Thr	Leu	Gln	Gly	Lys	Gln	Met
				95					100					105

His	Val	Gly	Lys	Thr	Pro	Ile	Gln	Val	Phe	Leu	Gly	Val	Pro	Phe
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Ser	Arg	Pro	Pro	Leu	Gly	Ile	Leu	Arg	Phe	Ala	Pro	Pro	Glu	Pro
				125					130					135

Pro Glu Pro Trp Lys Gly Ile Arg Asp Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu Ala Leu Ser Pro Gly Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr Ala Thr Ser Ala Ser Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro Leu Ser Val Trp Gly Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln Leu Ala Ser Met Tyr Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu Arg Phe Ser Glu Asp Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala Arg Ala Pro Gly Asp Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro Gly Gly Ala Phe Ile Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser Asp Leu Ala Ala Arg Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His Arg Leu Gly Ile Phe Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala Arg Gly Asn Trp Gly Leu Leu Asp Gln Met Ala	290	295	300
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Ile Ser Gly Leu Met Met Ser Pro Leu Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser Gln Ser Gly Thr Ala Leu Phe Arg Leu Phe Ile	350	355	360
Thr Ser Asn Pro Leu Lys Val Ala Lys Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His Asn Ser Thr Gln Ile Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly Thr Lys Val Met Arg Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu Asn Phe Gln Arg Asp Pro Glu Glu Ile Ile Trp	410	415	420

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Leu	Val	Leu	Leu	Thr	Gln	Gly	Lys	Val	Ser	Ser	Val	Pro	Tyr	Leu	
				440					445					450	
Leu	Gly	Val	Asn	Asn	Leu	Glu	Phe	Asn	Trp	Leu	Leu	Pro	Tyr	Asn	
				455					460					465	
Ile	Thr	Lys	Glu	Gln	Val	Pro	Leu	Val	Val	Glu	Glu	Tyr	Leu	Asp	
				470					475					480	
Asn	Val	Asn	Glu	His	Asp	Trp	Lys	Met	Leu	Arg	Asn	Arg	Met	Met	
				485					490					495	
Asp	Ile	Val	Gln	Asp	Ala	Thr	Phe	Val	Tyr	Ala	Thr	Leu	Gln	Thr	
				500					505					510	
Ala	His	Tyr	His	Arg	Glu	Thr	Pro	Met	Met	Gly	Ile	Cys	Pro	Ala	
				515					520					525	
Gly	His	Ala	Thr	Thr	Arg	Met	Lys	Ser	Thr	Cys	Ser	Trp	Ile	Leu	
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Pro	Gln	Glu	Trp	Ala											
				545											

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 257

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<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

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<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met
				20					25					30

Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr
				35					40					45

Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp
				50					55					60

Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr
				65					70					75

Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe
				80					85					90

Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile
				95					100					105

Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val
				110					115					120

Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe
				125					130					135

Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp
				140					145					150

His	Asn	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly
				155					160					165

Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro
				170					175					180

Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu
				185					190					195

Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys
				200					205					210

Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro
				215					220					225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390

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Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

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Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu  
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Val Lys Phe Gln

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<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagaggggtgc tgag 24

<210> 262

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 262

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<210> 263

<211> 2857

<212> DNA

<213> Homo sapiens

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tcgctttaaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350  
attagggctt ttaccatca aaatttttaa aagtgctaag gtgtattoga 2400  
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ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700  
cgagaaaatt taaaggagca aaaatttgca agtcaaatag aaatgtacaa 2750  
atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
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atttaaa 2857

<210> 264  
<211> 772  
<212> PRT  
<213> Homo sapiens

<400> 264

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				20					25					30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp	
				35					40					45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser	
				50					55					60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn	
				65					70					75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe	
				80					85					90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu	
				95					100					105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile	
				110					115					120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val	
				125					130					135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp	
				140					145					150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr	
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Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser	
				170					175					180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro	
				185					190					195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser	
				200					205					210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln	
				215					220					225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr	
				230					235					240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile	
				245					250					255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro	
				260					265					270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile	
				275					280					285	



Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln		350	355	360
Val	Glu	Asp	Val	Asp	Glu	Pro	Pro	Leu	Phe	Leu	Leu	Pro	Tyr	Tyr		365	370	375
Val	Phe	Glu	Val	Phe	Glu	Glu	Thr	Pro	Gln	Gly	Ser	Phe	Val	Gly		380	385	390
Val	Val	Ser	Ala	Thr	Asp	Pro	Asp	Asn	Arg	Lys	Ser	Pro	Ile	Arg		395	400	405
Tyr	Ser	Ile	Thr	Arg	Ser	Lys	Val	Phe	Asn	Ile	Asn	Asp	Asn	Gly		410	415	420
Thr	Ile	Thr	Thr	Ser	Asn	Ser	Leu	Asp	Arg	Glu	Ile	Ser	Ala	Trp		425	430	435
Tyr	Asn	Leu	Ser	Ile	Thr	Ala	Thr	Glu	Lys	Tyr	Asn	Ile	Glu	Gln		440	445	450
Ile	Ser	Ser	Ile	Pro	Leu	Tyr	Val	Gln	Val	Leu	Asn	Ile	Asn	Asp		455	460	465
His	Ala	Pro	Glu	Phe	Ser	Gln	Tyr	Tyr	Glu	Thr	Tyr	Val	Cys	Glu		470	475	480
Asn	Ala	Gly	Ser	Gly	Gln	Val	Ile	Gln	Thr	Ile	Ser	Ala	Val	Asp		485	490	495
Arg	Asp	Glu	Ser	Ile	Glu	Glu	His	His	Phe	Tyr	Phe	Asn	Leu	Ser		500	505	510
Val	Glu	Asp	Thr	Asn	Asn	Ser	Ser	Phe	Thr	Ile	Ile	Asp	Asn	Gln		515	520	525
Asp	Asn	Thr	Ala	Val	Ile	Leu	Thr	Asn	Arg	Thr	Gly	Phe	Asn	Leu		530	535	540
Gln	Glu	Glu	Pro	Val	Phe	Tyr	Ile	Ser	Ile	Leu	Ile	Ala	Asp	Asn		545	550	555
Gly	Ile	Pro	Ser	Leu	Thr	Ser	Thr	Asn	Thr	Leu	Thr	Ile	His	Val		560	565	570

Cys Asp Cys Gly Asp Ser Gly Ser Thr Gln Thr Cys Gln Tyr Gln  
575 580 585

Glu Leu Val Leu Ser Met Gly Phe Lys Thr Glu Val Ile Ile Ala  
590 595 600

Ile Leu Ile Cys Ile Met Ile Ile Phe Gly Phe Ile Phe Leu Thr  
605 610 615

Leu Gly Leu Lys Gln Arg Arg Lys Gln Ile Leu Phe Pro Glu Lys  
620 625 630

Ser Glu Asp Phe Arg Glu Asn Ile Phe Gln Tyr Asp Asp Glu Gly  
635 640 645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg  
650 655 660

Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser  
665 670 675

Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro  
680 685 690

Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu  
695 700 705

Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr  
710 715 720

Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser  
725 730 735

Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu  
740 745 750

Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly  
755 760 765

Ser Ala Val Gln Ser Asn Asn  
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<210> 265

<211> 349

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200  
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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ccgccttaa cttcctccgc ggggccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200  
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250  
cattctcgcc ttcctgggat ggatcggcgc catcgtcagc actgccctgc 300  
cccagtggag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350  
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gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450  
aagcaaccgc tgccttgatg gtgggttgca tcctcctggg agtgatagca 500  
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gttcaagaat tctatgaccc tatgacccca gtcaatgcca ggtacgaatt 700  
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aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000

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atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300  
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<210> 270  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 270  
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 Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
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Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
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 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200  
ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
tttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450  
gaccctatga cccagtc aa tgccaggtac gaatttggtc aggctctctt 500  
cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
gctgttctctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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tccagctggt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100

cntcagcact gccctgcccc agtggaggat ttactcctat nccggcnaca 150

acatcgtgac cgcccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200

tgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgctga 250

atctgagcag cacattgcaa gcaacccgtg ccttgatggt ggttggcatc 300

ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350

tgaagtgctt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400

gggggcgcga tatttcttct tgcaggctctg gctatttttag ttgccacagc 450

atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273  
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gatgaancgc gccatcntca gactccctgc cccatggaga tttnnccctat 100  
gctggcgaca acatcntgac ccccagccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac ccntgccctg atggtgggtg 250  
gcatcctcct gggagtata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattggggggc gcgatatttc ttcttgacag tctggctatt tnnngttgcc 400  
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450  
cccagtcaat gccaggtacg aatttgggtc ggctctcttc actggctggg 500  
ctgctgcttc tctctgcctt ctgggaggtg cctactttg ctgttcctgc 550  
ga 552

<210> 274  
<211> 526  
<212> DNA  
<213> Homo sapiens

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<220>  
<221> unsure  
<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
<223> unknown base

<400> 274  
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tgaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
caaccctgac cttgatggg ttggcatcct cctgggagtg atagcaacct 250  
ttgtggccac cgttggcatg aagtgtatga agtgcttgga agacgatgag 300  
gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
cnnngnntct atgacctat gacccagtc aatgccaggt acgaatttgg 450



tcaggetctc ttcactggct gggctgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

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gcagcacatt ncaagcaacc ccttgcccttg aagggtggtg ncatcccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300

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ctctctgcct tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<210> 276

<211> 495

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<223> unknown base

<400> 276

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ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgcgtgtcg 100

cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgcgatatctt cttnttgacg gtctggctat tttagttgcc acagcatggt 350

atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400

gccaggtagc aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

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cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtag gaatttgggc aggcctctntt cactggntgg 150

gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcctgggat ggatccgccc ccactntcac atgccctgcc ccttgagat 50

ttacncctat gctggcgaac aacatcntga ccgccaggc catgtacgag 100

gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtga 150

aagtctttga ctcttgctg aatctgagca gcacattga agcaaccntg 200

ccttgatggt gggtggcatc ctctgggag tgatagcaat ctttgtggcc 250

accgttgga tgaaagtga tgaagtgctt ggaagacgat gaggtgcaga 300

agatgaggat ggctgtcatt gggggcgcga tatttcttct tgcaggtctg 350

gctattttag nngccacagc atggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgaccca gtcaatgcca ggtaagaatt tggtcaggct 450

ctcttactg gctgggctgc tgcttctctc tgcttcttg gaggtgccct 500

actttgctgt tcctgtcccc gaaaaacaac ctcttaccga cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcattctgc ttcctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100  
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctcttgctg 200  
aatctgagca gcacattgca agcaaccntg ccttgatggg ggttggcatc 250  
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350  
ggggcgcgat atttcttctt gcaggtcttg ctatttntag ttgccacagc 400  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
tcaatgccag gtacgaattt ggtcaggctc tcttacttgg ctgggctgct 500  
gcttctctct gccttctggg aggtgcccta ctttgcgtgt cctgcgaa 548

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<210> 280  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 280  
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<210> 281  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 281  
gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
<211> 43

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 282  
ctgcagctgt tgggcttcat tctcgccttc ctgggatgga tcg 43

<210> 283  
<211> 2285  
<212> DNA  
<213> Homo sapiens

<400> 283  
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ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
tagaggaccc ccgcccgtgc cccgaccggt ccccgcttt ttgtaaaact 150  
taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
ctccccgcca aagggtgctc gccgctaagg aacatggcga aggtggagca 250  
ggctctgagc ctcgagccgc agcacgagct caaattccga ggtcccttca 300  
ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700  
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagtt aaaaatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaaggaa accatgagta atgccacaat ggcatattgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctcgctgtg tgggtgctggc ccttggggag 1350  
ctggagccca gcatgctggg gaggcggtc agtccacac agtagtccc 1400  
acgtggccca ctcccgccc aggtgcttt ccgtgtcttc agttctgtcc 1450  
aagccatcag ctcttgga ctgatgaaca gagtcagaag ccaaaggaa 1500  
ttgcaactgtg gcagcatcag acgtactcgt cataagtga aggcgtgtgt 1550  
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taaagggacc aagctaaatt tgtattggt catgtagtga agtcaaactg 1650  
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcact 1700  
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750  
ctctgttggg tgaactgta ttgctgctgg agggctgtgg gctcctctgt 1800  
ctctggagag tctggatcag tggaggtgg gtttattggg atgctggaga 1850  
agagctgcca ggaagtgtt tttctgggtc agtaaataac aactgtcata 1900

gggagggaaa ttctcagtag tgacagtcaa ctctaggta ctttttttaa 1950  
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050  
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggtagaa 2100  
gagagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag tttgactgtg aattaatttt 2200  
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250  
agaaaaatta taataaagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
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Lys Leu Gly Asn Pro	Thr Asp Arg Asn	Val Cys Phe Lys	Val Lys
35		40	45
Thr Thr Ala Pro Arg	Arg Tyr Cys Val	Arg Pro Asn Ser	Gly Ile
50		55	60
Ile Asp Ala Gly Ala	Ser Ile Asn Val	Ser Val Met Leu	Gln Pro
65		70	75
Phe Asp Tyr Asp Pro	Asn Glu Lys Ser	Lys His Lys Phe	Met Val
80		85	90
Gln Ser Met Phe Ala	Pro Thr Asp Thr	Ser Asp Met Glu	Ala Val
95		100	105
Trp Lys Glu Ala Lys	Pro Glu Asp Leu	Met Asp Ser Lys	Leu Arg
110		115	120
Cys Val Phe Glu Leu	Pro Ala Glu Asn	Asp Lys Pro His	Asp Val
125		130	135
Glu Ile Asn Lys Ile	Ile Ser Thr Thr	Ala Ser Lys Thr	Glu Thr
140		145	150
Pro Ile Val Ser Lys	Ser Leu Ser Ser	Ser Leu Asp Asp	Thr Glu
155		160	165
Val Lys Lys Val Met	Glu Glu Cys Lys	Arg Leu Gln Gly	Glu Val
170		175	180
Gln Arg Leu Arg Glu	Glu Asn Lys Gln	Phe Lys Glu Glu	Asp Gly
185		190	195
Leu Arg Met Arg Lys	Thr Val Gln Ser	Asn Ser Pro Ile	Ser Ala
200		205	210
Leu Ala Pro Thr Gly	Lys Glu Glu Gly	Leu Ser Thr Arg	Leu Leu
215		220	225
Ala Leu Val Val Leu	Phe Phe Ile Val	Gly Val Ile Ile	Gly Lys
230		235	240
Ile Ala Leu			

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

gtcagttctt tagattgtcc ttatcccacc tttcaaccan tactcacatt 50  
tenagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
cagcagtttt ggggtggggag caagggnga gagaaactct tcagcgaatc 200  
cttctagtac tagttgagag tttgactgtg aattaatttt atgccataaa 250  
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350  
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaag gccattttaa accattggta ggccttggtg catgatgctg 50  
gattacctcc ttaaattgaca ccttcctcg cctgttggtg ctggccttg 100  
gggagctgga gccccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagcca 250  
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcttt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata tttaacttat ttaatgtatt 450  
tcatctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242  
<223> unknown base

<400> 287  
ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50  
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288  
<211> 428  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351  
<223> unknown base

<400> 288  
gggtggcccat tcccggccca ggctgctttc cggtnctcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcttt ggaaataaat ggcaagtgtt tgttcantta 200  
aagggaacaa gctaaatttg tattggttca ttagtgtaag tcaaactgtt 250  
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttggttg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289  
<211> 320  
<212> DNA  
<213> Homo sapiens

<400> 289  
tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50



atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
tactcgtcat aagtgaagagg cgtgtgttga ctgattgacc cagcgctttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcattcat gttttcttat tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290  
<211> 609  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598  
<223> unknown base

<400> 290  
aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaaccntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100  
ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150  
cttctctgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200  
ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
cccaggctgc tttccgtgct ttcagttctg tccaagccat cagctccttg 300  
ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
cagangtant ngcataagt gagaggcgtg tgttgantga ttgaccagc 400  
gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
atgcatattt aantattta atgtatttca tntcatgttt tcttattgtc 550  
acaagggtag agttaatgct gcgtgctgct gaantctgtt ggggtgaantg 600  
gtattgctg 609

<210> 291  
<211> 493  
<212> DNA  
<213> Homo sapiens

<400> 291

ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50  
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ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250  
tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300  
tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400  
gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450  
tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgaggc 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150  
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200  
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250  
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300  
atctttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350  
atcttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400  
ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450  
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cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600  
aaatatcacc acaaaggag tatctgttag gagaaagaga caggtgtatg 650  
gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700  
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750  
ttcccctcag catgttctaa ctgctgcca ctgtgttcat gatggaaagg 800

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actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850  
aataaaagtg gaggaagaa acgtcgaggt tctaagagga gcaggagaga 900  
agctagtggg ggtgaccaa gagagggtac cagagagcat ctgcaggaga 950  
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000  
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tccgaagggc tgggcacgag gaggcattgg ggacgctacc ttggactatg 1100  
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cttggaatca gccaacgat caagaaaatg cctggtggaa tgatccactt 1200  
ctcaggatth gataacgata gggctgatca gttggtctat cggttttgca 1250  
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tcgggctcca ccggttcggg ggtctatctg cgtctgaaag atccagacaa 1350  
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 ttgtgcttac ggctaacaga gacctgaaac agggcggtgt atcatctaaa 1550  
 tcacagagaa aaccagctct gcttaccgta gtgagatcac ttcatagggt 1600  
 atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaaatca 1650  
 ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700  
 gtggggcactt caatgccaaag tatatactct tctttacatg gtgatgagtt 1750  
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 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850  
 ctcagggtcc tactctaaga agaactaat aggatgctgg ttgtgtatta 1900  
 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950  
 atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000  
 ttcagctcat gccctcaatg tttatattgt gttatctggt gggctctggga 2050  
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100  
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150  
 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200

cctagttagt aaatagggaa gctgagacat tttaagatct caagtittta 2250  
 tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300  
 cttcaciaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450  
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500  
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
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Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

20										25					30				
Leu	Arg	Lys	Val	Pro	Arg	Ile	Val	Ser	Glu	Arg	Thr	Phe	His	Leu					
				35					40					45					
Thr	Ser	Pro	Ala	Phe	Glu	Ala	Asp	Ala	Lys	Met	Met	Val	Asn	Thr					
				50					55					60					
Val	Cys	Gly	Ile	Glu	Cys	Gln	Lys	Glu	Leu	Pro	Thr	Pro	Ser	Leu					
				65					70					75					
Ser	Glu	Leu	Glu	Asp	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Phe	Glu	Asn					
				80					85					90					
Gly	Thr	Arg	Thr	Leu	Thr	Arg	Val	Lys	Val	Gln	Asp	Leu	Val	Leu					
				95					100					105					
Glu	Pro	Thr	Gln	Asn	Ile	Thr	Thr	Lys	Gly	Val	Ser	Val	Arg	Arg					
				110					115					120					
Lys	Arg	Gln	Val	Tyr	Gly	Thr	Asp	Ser	Arg	Phe	Ser	Ile	Leu	Asp					
				125					130					135					
Lys	Arg	Phe	Leu	Thr	Asn	Phe	Pro	Phe	Ser	Thr	Ala	Val	Lys	Leu					
				140					145					150					
Ser	Thr	Gly	Cys	Ser	Gly	Ile	Leu	Ile	Ser	Pro	Gln	His	Val	Leu					
				155					160					165					
Thr	Ala	Ala	His	Cys	Val	His	Asp	Gly	Lys	Asp	Tyr	Val	Lys	Gly					
				170					175					180					
Ser	Lys	Lys	Leu	Arg	Val	Gly	Leu	Leu	Lys	Met	Arg	Asn	Lys	Ser					
				185					190					195					
Gly	Gly	Lys	Lys	Arg	Arg	Gly	Ser	Lys	Arg	Ser	Arg	Arg	Glu	Ala					
				200					205					210					
Ser	Gly	Gly	Asp	Gln	Arg	Glu	Gly	Thr	Arg	Glu	His	Leu	Gln	Glu					
				215					220					225					
Arg	Ala	Lys	Gly	Gly	Arg	Arg	Arg	Lys	Lys	Ser	Gly	Arg	Gly	Gln					
				230					235					240					
Arg	Ile	Ala	Glu	Gly	Arg	Pro	Ser	Phe	Gln	Trp	Thr	Arg	Val	Lys					
				245					250					255					
Asn	Thr	His	Ile	Pro	Lys	Gly	Trp	Ala	Arg	Gly	Gly	Met	Gly	Asp					
				260					265					270					
Ala	Thr	Leu	Asp	Tyr	Asp	Tyr	Ala	Leu	Leu	Glu	Leu	Lys	Arg	Ala					
				275					280					285					
His	Lys	Lys	Lys	Tyr	Met	Glu	Leu	Gly	Ile	Ser	Pro	Thr	Ile	Lys					
				290					295					300					
Lys	Met	Pro	Gly	Gly	Met	Ile	His	Phe	Ser	Gly	Phe	Asp	Asn	Asp					

	305		310		315
Arg Ala Asp Gln	Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp	Glu		
	320	325	330		
Ser Asn Asp Leu	Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly	Ser		
	335	340	345		
Thr Gly Ser Gly	Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys	Lys		
	350	355	360		
Asn Trp Lys Arg	Lys Ile Ile Ala Val	Tyr Ser Gly His Gln	Trp		
	365	370	375		
Val Asp Val His	Gly Val Gln Lys Asp	Tyr Asn Val Ala Val	Arg		
	380	385	390		
Ile Thr Pro Leu	Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His	Gly		
	395	400	405		
Asn Asp Ala Asn	Cys Ala Tyr Gly				
	410				

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catcggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggaggc cttcctttca gtggaccgg gtcaagaata cccac 45

<210> 300

<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300

aatgtgagag gggctgatgg aagctgatag gcaggactgg agtgtttagca 50  
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gcccattggag tgaatgctca cgcacctgcg ggggaggggc ctctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgcccacc agaagcaggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500  
ccaagccaaa ggaacaacc tggttggtga actagcacct aaggcttag 550  
atggtacgcg ttgctataca gaatctttgg atatgtgcat cagtggttta 600  
tgccaaattg ttggctgcca tcaccagctg ggaagcaccg tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctggtccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcggatga tactgtggtt 750  
gcacttcctt atggaagtag acatattcgc cttgtcttaa aaggctcctga 800  
tcacttatat ctggaacca aaaccctcca ggggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttggtg acaattctag tgtggacttc 900  
cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950  
agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000  
agttcatctt ctatcaacc atcatccacc gatggaggga gacggatttc 1050  
tttccttgct cagcaacctg tggaggaggt tatcagctga catcggctga 1100  
gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150  
attaccaga gaacatcaaa cccaaacca agcttcagga gtgcaacttg 1200  
gatccttgct cagccagtga cggatacaag cagatcatgc cttatgacct 1250  
ctaccatccc cttcctcggg gggaggccac cccatggacc gcgtgctcct 1300

cctcgtgtgg ggggggcatc cagagccggg cagtttcctg tgtggaggag 1350  
 gacatccagg ggcattgtcac ttcatgtgaa gaggaggaaat gcatgtacac 1400  
 ccctaagatg cccatcgcgc agccctgcaa cttttttgac tggcctaaat 1450  
 ggctggcaca ggagtgggtct ccgtgcacag tgacatgtgg ccagggcctc 1500  
 agataccgtg tggtcctctg catcgacat cgaggaatgc acacaggagg 1550  
 ctgtagccca aaaacaaagc cccacataaa agaggaatgc atcgtaccca 1600  
 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650  
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700  
 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750  
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800  
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850  
 ttagtttcaa aaaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301

Met	Glu	Cys	Cys	Arg	Arg	Ala	Thr	Pro	Gly	Thr	Leu	Leu	Leu	Phe
1				5					10					15

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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30

Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45

Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60

Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75

Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala
			80						85					90

Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105

Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120

Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135



Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
<del>Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly</del>	<del>305</del>	<del>310</del>	<del>315</del>
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctgggcgggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccgc cctcatgcac gggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgccgag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcggcggtc agctccgccg cgagctccgc caggccgcgg 350  
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgct gcgctcgtg cgcgccttct gccaggaaat 450  
 gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtgcc cttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagttca gctcccagca ggattgtggg agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750

ggaactagcc cgccgcttag aaggcacaaa tgtcacccgtc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacatata cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaactcc 900  
 agtagaaggt gccagactt ccattttattt ggctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggt ggctgtctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatgggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350  
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttgggtgtt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttggaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
1				5					10				15	

Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25					30

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35					40					45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50					55					60

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65					70					75

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80					85					90

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Glu Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304

<211> 521

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 20, 34, 62, 87, 221, 229

<223> unknown base

<400> 304

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gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttgagatt 250  
actgaaaaat tatttttggg ataagagaat ttcagcaaag atgtttttaa 300  
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
attgtaaaat tataactggg caagcatgga tgacatatta atatgtgtca 400  
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
tggaattat ctgcctggct t 521

<210> 305

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 305

ccaggaaatg ctccaggaag agcc 24

<210> 306

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 306

gcccatgaca ccaaattgaa gagtgg 26

<210> 307

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 307

aacgcagggg tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaacca acctagccca gtcccagccg 100  
ccagcgcctg tccctgtcac ggacccagc gttaccatgc atcctgccgt 150  
cttcctatcc ttacccgacc tcagatgctc cttctgctc ctggttaactt 200  
gggtttttac tctgttaaca actgaaataa caagtcttg tacagagaat 250  
atagatgaaa ttttaacaa tgctgatgtt gctttagtaa atttttatgc 300  
tgactgggtg cgtttcagtc agatgttgca tccaatttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 450  
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650

cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050  
acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcat atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250

gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttccag 1300  
 aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
 gcttttaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
 cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
 tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
 <211> 406  
 <212> PRT  
 <213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser
1				5					10					15

Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu
				20					25					30

Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn
				35					40					45

Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe
				50					55					60

Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile
				65					70					75

Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val
				80					85					90

Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser
				95					100					105

Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys
				110					115					120

Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr
				125					130					135

Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Glu	Ile	Arg	Asp	Leu
				140					145					150

Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly
				155					160					165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170					175					180

Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185					190					195

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360

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His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 48  
 <223> unknown base

<400> 310



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ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311

<211> 598

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396

<223> unknown base

<400> 311

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gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 100  
cggagcccag ccttttcta acccaacca acctagcccn gtcccagccg 150  
ccagcgcctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttcctatcc ttacccgacc tcagatgctc ctttctgctc ctggtaactt 250  
gggtttttac tcctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaacna tgctgatgtg gcttttagtca atttttatgc 350

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tgactgggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaa atgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 312

tgagaggcct ctctggaagt tg 22

<210> 313

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

ggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 318  
ctgtatctct gggctatgtc agag 24

<210> 319  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 319  
ctacatataa tggcacatgt cagcc 25

<210> 320  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 320  
cgtcttccta tccttaccgc acctcagatg ctcccttctg ctcttg 46

<210> 321  
<211> 1333  
<212> DNA  
<213> Homo sapiens

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<400> 321  
gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50  
cgctgctgct cactgccgcg ctcatcttct tcgccatttg gcacattata 100  
gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150  
taccctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200  
gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250  
cccctcttgg catatcatat ttggaggat atgagtagac cagtgatgag 300  
tggtccagga ctctatgacc ctacaaccat catgaatgca gatattctag 350  
catattgtca gaaggaagga tgggtgcaat tagcttttta tcttctagca 400  
tttttttact acctatatgg catgatctat gttttgggtga gctcttagaa 450  
caacacacag aagaattggc ccagttaagt gcatgcaaaa agccacaaa 500  
tgaagggtt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550  
tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttccacat 600

ttttgcttgt ggaaagactg ttttcatatg ttataactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatataa atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcagggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcactctgc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt ctttaagcata agtaaacaatg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaattgtgt 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactctg gtggtaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
1				5				10					15	

Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20				25					30	

Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35				40					45	

Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50				55					60	

Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65				70					75	

Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80				85					90	

Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95				100					105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
tgtaataccc tgaatcccct tgtactccca gaggtaacctca tccacgcttt 100  
cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150  
atatgcccct cttggcatat catatttga ggtatatgag tagaccagt 200  
atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
tctagcatat tgcagaagg aaggatgggtg caaattagct ttttatcttc 300  
tagcattttt ttactaccta tatggcatga tctatgtttt ggtgagctct 350  
tagaacaaca cacagaagaa ttggtccagt taagtgcattg caaaaagcca 400  
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450

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gaatctgatc agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaat tagct 45

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<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggaccaact ggggctcccg ccgctgctgc tgctgacat ggccttggcc 150  
ggaggttcgg ggaccgcttc ggctgaagca tttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagaggttg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaata gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaatct gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450

caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttcctct 500  
 aactctgggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
 tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
 gttatatcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
 ggagcctaca aatttgagag aatcatctct aagcaaatg tcctatctgc 700  
 aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
 gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
 aactcttgct ctctcggtga tggatttgct ttggatttgc tgtgcaactg 850  
 ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900  
 ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
 ttctcttggt gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
 ctctacctac aaaagtgaat cttgctcatt ctgaaattta agcatttttc 1050  
 ttttaaaaga caagtgaat agacatctaa aattocactc ctcatagagc 1100  
 ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
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<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
				20					25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
				35					40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
				50					55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
				65					70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
				80					85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
				95					100					105

Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln	
				110						115				120	
Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125						130				135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140						145				150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155						160				165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170						175				180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185						190				195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200						205				210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215						220				225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230						235				240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245						250				255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260						265				270	

Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275						280				285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290						295				300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305						310				315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331

<211> 350

<212> DNA

<213> Homo sapiens

<400> 331

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gcacacctac cctaaggaag aggagttgta cgcattgtcag agaggttgca 100

ggctgttttc aatttgctcag tttgtggatg atggaattga cttaaatacga 150



actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200  
tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250  
aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
tttctcttaa ctctggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
<211> 562  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 47  
<223> unknown base

<400> 332  
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aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100  
cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150  
tgctgaccat ggccttggcc ggagggttcgg ggaccgcttc ggctgaagca 200  
tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250  
gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350

gacttaaadc gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400  
ttcccaatct gatgagcaat atgcttgcca tcttgggtgc cagaatcagc 450  
tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550  
gatggactcc gc 562

<210> 333  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 333  
acaagctgag ctgctgtgac ag 22

<210> 334  
<211> 22

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggttc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgaggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cgggcccgag gtggggcgcc gctggggccg gcccgcacgg gttcatctg 100  
aggggcgacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatgggccg cggctgggga ttctgtttg 200

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gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgaga cagcggcaca gaggtgcttc tgccagggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaaccat tgatagattt aataactaca 350  
ggcttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggctgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800

agccacagac aattaaaga cctttaaatc ctttggcttc tggcgaagg 850  
 acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
 aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950  
 tgcatttgag tgcaagatat cttttacaag agacctggtt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatttt ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttcga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaatgtt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgctggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaactttt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaaaa 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
 1 5 10 15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
 20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
35 40 45

Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
50 55 60

Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
65 70 75

Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp  
80 85 90

Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln  
95 100 105

Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr  
110 115 120

Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu  
125 130 135

Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys  
140 145 150

Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe  
155 160 165

Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp  
170 175 180

Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp  
185 190 195

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Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys  
200 205 210

Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln  
215 220 225

Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu  
230 235 240

Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu His  
245 250 255

Ala Ser Ile Asn Val His Leu Ser Ala Arg Tyr Leu Leu Gln Glu  
260 265 270

Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln  
275 280 285

Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg  
290 295 300

Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu  
305 310 315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	
				320					325					330	
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	
				335					340					345	
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	
				350					355					360	
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	
				365					370					375	
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	
				380					385					390	
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	
				395					400					405	
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	
				410					415					420	
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	
				425					430					435	
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	
				440					445					450	
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	
				455					460					465	
Asn	Ile	His													

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
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 ttaaaagacc tttaaactct ttggcttctg gtcaaggac aagtgaagag 100  
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct ttacaagag acctggtag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350

ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400  
actggaaata aaattcagga tgaggnaaac aaaatgttac ttttggaat 450  
acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500  
tttgetg 507

<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

aagctgccgg agctgcaatg 20

<210> 340

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 342

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<210> 343

<211> 25

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tgggacggac cgtgggttg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagaggac agaggccaga 100

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cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

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gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

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aaagagaagt gtggttaagg aaaatggtct gtgtggagg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

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<210> 346

<211> 124

<212> PRT

<213> Homo sapiens

<400> 346

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Arg	Leu	Phe	Pro	Gly	Pro	Pro	Glu	Ala	Glu	Phe	Gly	Tyr	Ser	Val	35	40	45	
Leu	Gln	His	Val	Gly	Gly	Gly	Gln	Arg	Trp	Met	Leu	Val	Gly	Ala	50	55	60	
Pro	Trp	Asp	Gly	Pro	Ser	Gly	Asp	Arg	Arg	Gly	Asp	Val	Tyr	Arg	65	70	75	
Cys	Pro	Val	Gly	Gly	Ala	His	Asn	Ala	Pro	Cys	Ala	Lys	Gly	His	80	85	90	
Leu	Gly	Asp	Tyr	Gln	Leu	Gly	Asn	Ser	Ser	His	Pro	Ala	Val	Asn	95	100	105	
Met	His	Leu	Gly	Met	Ser	Leu	Leu	Glu	Thr	Asp	Gly	Asp	Gly	Gly	110	115	120	



Phe Met Val Ser

<210> 347  
<211> 509  
<212> DNA  
<213> Homo sapiens

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<222> 22  
<223> unknown base

<400> 347  
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ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgtcct 200  
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aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggcccaca 400  
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
tctcatcctg ctgtgaatat gcacctggg atgtctctgt tagagacaga 500

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tggtgatgg 509

<210> 348  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 348  
agggacagag gccagaggac ttc 23

<210> 349  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 349  
caggtgcata ttcacagcag gatg 24

<210> 350  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 350  
ggaactcccc ttcgtcactc acctgttctt gcccctgggtg ttcct 45

<210> 351  
<211> 2056  
<212> DNA  
<213> Homo sapiens

<400> 351  
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gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctacaaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
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 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
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 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
 20 25 30

Glu	Val	Ala	Ile	Leu 35	Pro	Ala	Pro	Gln	Asn 40	Leu	Ser	Val	Leu	Ser 45
Thr	Asn	Met	Lys	His 50	Leu	Leu	Met	Trp	Ser 55	Pro	Val	Ile	Ala	Pro 60
Gly	Glu	Thr	Val	Tyr 65	Tyr	Ser	Val	Glu	Tyr 70	Gln	Gly	Glu	Tyr	Glu 75
Ser	Leu	Tyr	Thr	Ser 80	His	Ile	Trp	Ile	Pro 85	Ser	Ser	Trp	Cys	Ser 90
Leu	Thr	Glu	Gly	Pro 95	Glu	Cys	Asp	Val	Thr 100	Asp	Asp	Ile	Thr	Ala 105
Thr	Val	Pro	Tyr	Asn 110	Leu	Arg	Val	Arg	Ala 115	Thr	Leu	Gly	Ser	Gln 120
Thr	Ser	Ala	Trp	Ser 125	Ile	Leu	Lys	His	Pro 130	Phe	Asn	Arg	Asn	Ser 135
Thr	Ile	Leu	Thr	Arg 140	Pro	Gly	Met	Glu	Ile 145	Thr	Lys	Asp	Gly	Phe 150
His	Leu	Val	Ile	Glu 155	Leu	Glu	Asp	Leu	Gly 160	Pro	Gln	Phe	Glu	Phe 165
Leu	Val	Ala	Tyr	Trp 170	Arg	Arg	Glu	Pro	Gly 175	Ala	Glu	Glu	His	Val 180
Lys	Met	Val	Arg	Ser 185	Gly	Gly	Ile	Pro	Val 190	His	Leu	Glu	Thr	Met 195
Glu	Pro	Gly	Ala	Ala 200	Tyr	Cys	Val	Lys	Ala 205	Gln	Thr	Phe	Val	Lys 210
Ala	Ile	Gly	Arg	Tyr 215	Ser	Ala	Phe	Ser	Gln 220	Thr	Glu	Cys	Val	Glu 225
Val	Gln	Gly	Glu	Ala 230	Ile	Pro	Leu	Val	Leu 235	Ala	Leu	Phe	Ala	Phe 240
Val	Gly	Phe	Met	Leu 245	Ile	Leu	Val	Val	Val 250	Pro	Leu	Phe	Val	Trp 255
Lys	Met	Gly	Arg	Leu 260	Leu	Gln	Tyr	Ser	Cys 265	Cys	Pro	Val	Val	Val 270
Leu	Pro	Asp	Thr	Leu 275	Lys	Ile	Thr	Asn	Ser 280	Pro	Gln	Lys	Leu	Ile 285
Ser	Cys	Arg	Arg	Glu 290	Glu	Val	Asp	Ala	Cys 295	Ala	Thr	Ala	Val	Met 300
Ser	Pro	Glu	Glu	Leu 305	Leu	Arg	Ala	Trp	Ile 310	Ser				

<210> 353  
<211> 864  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 654, 711, 748, 827  
<223> unknown base

<400> 353  
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200  
ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250  
tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
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cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
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gaacccttg cgccgctgg ggtatctctc gagaaaagag aggcccaata 800  
tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
ggcgtgggt tgat 864

<210> 354  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 354  
aggcttcgct gcgactagac ctc 23

<210> 355  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 355  
ccaggtcggg taaggatggt tgag 24

<210> 356  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
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<212> DNA  
<213> Homo sapiens

<400> 357  
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acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100

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ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<400> 358

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				20					25					30

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
				35					40					45

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
				50					55					60

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75

Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90

Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105

His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120

Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135

Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150

His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165

Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly  
170 175 180

Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn  
185 190 195

Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile  
200 205 210

Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu  
215 220 225

Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser  
230 235 240

Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile  
245 250 255

Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg  
260 265 270

Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser  
275 280 285

Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg  
290 295 300

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305 310 315

Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg  
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<210> 359

<211> 24



<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 359  
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<210> 360  
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<400> 360  
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<210> 361  
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<210> 362  
<211> 3038

<212> DNA  
<213> Homo sapiens

<400> 362  
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<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
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Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
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Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu			
				245					250					255			
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
500	

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365  
ccaagagtat actgtcctcg 20

<210> 366  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 366  
agcacagatt ttctctacag ccccc 25

<210> 367  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 367  
aaccactcca gcatgtactg ctgc 24

<210> 368  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

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<400> 368  
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<210> 369  
<211> 1685  
<212> DNA  
<213> Homo sapiens

<400> 369  
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agagaaagcc gagcagagct ggggtggcgtc tccgggccgc cgctccgacg 150  
ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200  
gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250  
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gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtag 400  
cgaggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450  
catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500  
agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550  
gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600  
aaaaaaaaaa aaagcctttt tttctcacag gcataagaca caaattatat 650  
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gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750  
ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800  
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cagtgttgcct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950  
gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000  
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ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

Met	Ser	Leu	Leu	Pro	Arg	Arg	Ala	Pro	Pro	Val	Ser	Met	Arg	Leu
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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20					25					30
Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35					40					45
Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50					55					60
Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65					70					75
Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80					85					90
Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95					100					105
Arg	Arg	Val	Tyr	Glu	Glu									
				110										

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> ~~Synthetic oligonucleotide probe~~

<400> 371

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<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 373  
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<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

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accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150  
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200  
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<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

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Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
				20					25					30
Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
				35					40					45
Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
				50					55					60
Ser	Pro	Pro	Thr	Gly	Glu	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Pro	Pro
				65					70					75
Ser	Ser	Trp	Thr	Gly	Ile	Arg	Asn	Thr	Thr	Gln	Phe	Ala	Ala	Val
				80					85					90
Cys	Pro	Gln	His	Leu	Asp	Glu	Arg	Ser	Leu	Leu	His	Asp	Met	Leu
				95					100					105
Pro	Ile	Trp	Phe	Thr	Ala	Asn	Leu	Asp	Thr	Leu	Met	Thr	Tyr	Val
				110					115					120
Gln	Asp	Gln	Asn	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Ile	Tyr	Val	Pro
				125					130					135
Thr	Glu	Asp	Gly	Ala	Asn	Thr	Lys	Lys	Asn	Ala	Asp	Asp	Ile	Thr
				140					145					150

Ser	Asn	Asp	Arg	Gly	Glu	Asp	Glu	Asp	Ile	His	Asp	Gln	Asn	Ser			
				155					160					165			
Lys	Lys	Pro	Val	Met	Val	Tyr	Ile	His	Gly	Gly	Ser	Tyr	Met	Glu			
				170					175					180			
Gly	Thr	Gly	Asn	Met	Ile	Asp	Gly	Ser	Ile	Leu	Ala	Ser	Tyr	Gly			
				185					190					195			
Asn	Val	Ile	Val	Ile	Thr	Ile	Asn	Tyr	Arg	Leu	Gly	Ile	Leu	Gly			
				200					205					210			
Phe	Leu	Ser	Thr	Gly	Asp	Gln	Ala	Ala	Lys	Gly	Asn	Tyr	Gly	Leu			
				215					220					225			
Leu	Asp	Gln	Ile	Gln	Ala	Leu	Arg	Trp	Ile	Glu	Glu	Asn	Val	Gly			
				230					235					240			
Ala	Phe	Gly	Gly	Asp	Pro	Lys	Arg	Val	Thr	Ile	Phe	Gly	Ser	Gly			
				245					250					255			
Ala	Gly	Ala	Ser	Cys	Val	Ser	Leu	Leu	Thr	Leu	Ser	His	Tyr	Ser			
				260					265					270			
Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile	Ile	Gln	Ser	Gly	Thr	Ala	Leu			
				275					280					285			
Ser	Ser	Trp	Ala	Val	Asn	Tyr	Gln	Pro	Ala	Lys	Tyr	Thr	Arg	Ile			
				290					295					300			
Leu	Ala	Asp	Lys	Val	Gly	Cys	Asn	Met	Leu	Asp	Thr	Thr	Asp	Met			
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Val	Glu	Cys	Leu	Arg	Asn	Lys	Asn	Tyr	Lys	Glu	Leu	Ile	Gln	Gln			
				320					325					330			
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Glu	Gly	Leu	Lys	Phe	Val	Asp	Gly	Ile	Val	Asp	Asn	Glu	Asp	Gly			
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Val	Thr	Pro	Asn	Asp	Phe	Asp	Phe	Ser	Val	Ser	Asn	Phe	Val	Asp			
				395					400					405			
Asn	Leu	Tyr	Gly	Tyr	Pro	Glu	Gly	Lys	Asp	Thr	Leu	Arg	Glu	Thr			
				410					415					420			
Ile	Lys	Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Lys	Glu	Asn	Pro	Glu			
				425					430					435			

Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
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Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His	Ser Lys Asp Pro His	Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu	Ile Glu Thr Lys Arg	Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile	Ala Val Gly Ala Ser	Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala	Ala Leu Tyr Tyr Lys	Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg	Arg Pro Ser Pro Gln	Arg Asn Thr Thr Asn Asp	710	715	720

Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys  
725 730 735

Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp  
740 745 750

Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg  
755 760 765

Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr  
770 775 780

Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe  
785 790 795

Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly  
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<210> 377

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 47

<212> DNA

<213> Artificial Sequence

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<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

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 <212> PRT  
 <213> Homo sapiens

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Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met		65	70	75
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp		80	85	90
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Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln		110	115	120
Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr		125	130	135
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys		140	145	150
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu		155	160	165
Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn		170	175	180
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Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val		230	235	240
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser		245	250	255
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Asp	Val	Ile	Ser	Leu	Lys		260	265	270
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu		275	280	285
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro		290	295	300
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe		305	310	315

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val  
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<400> 382  
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
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Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
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Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
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Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
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Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
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Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
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Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
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Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
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Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
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Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
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Arg	Asp	Ile	Tyr	Leu	Lys	Lys	His	Lys	Leu	Leu	Pro	Asn	Asp	Trp
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Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
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Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys	Ser	Gly	Ser	Cys	Tyr	Cys	Pro	Val	Arg	Asn	Gln	Tyr	Leu	Glu	
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Lys	Glu	Gln	Arg	Arg	Gln	Tyr	Leu	Leu	Arg	Leu	Lys	Asn	Ser	Gln	
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His	Phe	Cys	His	Asn	Val	Ser	Phe	Pro	Cys	Thr	Arg	Asn	Gly	Cys	
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Asp	Glu	Arg	Glu	Arg	Arg	Glu	Lys	Lys	Leu	Tyr	Phe	Gly	Tyr	Ser	
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Gln	Arg	Ala	Thr	Glu	Gly	Arg	Lys	Glu	Glu	Leu	Phe	Ala	Leu	Tyr	
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Ser	Ala	His	Asp	Val	Thr	Leu	Ser	Pro	Val	Leu	Ser	Ala	Leu	Gly	
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Leu	Ser	Glu	Ala	Arg	Phe	Pro	Arg	Phe	Ala	Ala	Arg	Leu	Ile	Phe	
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Glu	Leu	Trp	Gln	Asp	Arg	Glu	Lys	Pro	Ser	Glu	His	Ser	Val	Arg	
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Ile	Leu	Tyr	Asn	Gly	Val	Asp	Val	Thr	Phe	His	Thr	Ser	Phe	Cys	
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Gln	Asp	His	His	Lys	Arg	Ser	Pro	Lys	Pro	Met	Cys	Pro	Leu	Glu	
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Asn	Leu	Val	Arg	Phe	Val	Lys	Arg	Asp	Met	Phe	Val	Ala	Leu	Gly	
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<211> 24

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<213> Artificial Sequence

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<210> 390

<211> 916

<212> PRT

<213> Homo sapiens

<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln		20	25	30	
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val		35	40	45	
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala		50	55	60	
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe		65	70	75	
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile		80	85	90	
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn		95	100	105	
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu		110	115	120	
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu		125	130	135	
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met		140	145	150	
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn		155	160	165	
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu		170	175	180	
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val		185	190	195	
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu		200	205	210	
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr		215	220	225	
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro		230	235	240	
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu		245	250	255	
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp		260	265	270	
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp		275	280	285	

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Phe Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly  
575 580 585

Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln  
590 595 600

Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly  
605 610 615

Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg  
620 625 630

Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala  
635 640 645

Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu  
650 655 660

Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu  
665 670 675

Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr  
680 685 690

Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu  
695 700 705

Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His  
710 715 720

Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala  
725 730 735

Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu  
740 745 750

Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys  
755 760 765

Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val  
770 775 780

Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly  
785 790 795

Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser  
800 805 810

Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser  
815 820 825

Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln  
830 835 840

Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn  
845 850 855

Arg Asp Tyr Arg Cys Lys Pro Pro Thr Val Cys Leu Ser Ile Tyr  
860 865 870

Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Ser Ile Tyr Leu Leu Leu  
875 880 885

Ser Cys Thr Asp Gly Ser Leu Thr Pro Val Ile Pro Val Leu Trp  
890 895 900

Glu Ala Glu Ala Gly Gly Ser Pro Glu Val Gly Ser Leu Arg Pro  
905 910 915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

tccgtctctg tgaaccgccc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<400> 392

ctcgggcgca ttgtcgttct ggtc 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccgactgtga aagagaacgc cccagatcca cttgttcccc 40

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50

cccaggtaaa aggctccaga atcgtgtacc aggagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150  
 ctggaagacc tcaccatggg acgccccga cctcgtgcg ccaagacgtg 200  
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
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 caagaaatac ctgtggttca gtccatccca caccctgct acaacagcag 500  
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<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
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Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn  
80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro  
95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp  
110 115 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys  
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln  
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu  
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro  
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly  
185 190 195

Met Val Cys Ala Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly  
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile  
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly  
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile  
245 250 255

Ile Gly Ser Lys Gly  
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<210> 396

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 396

cagcctacag aataaagatg gccc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga tctgccaggc tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

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cgccgcgagg ccccgcccc gccgccccc gcccgcccc ggccggcggg 200

ggaagcgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcatectccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgcctcgc cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggcgga gcggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtag cggcggcgcc tggatgcgga cccggccgcg 450

gggagacggg cgcgcgcccc gaaacgactt tcagtcccc acgcgccccg 500

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 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
				50					55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
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Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val  
275 280 285

Pro Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg  
290 295 300

Leu Ala Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro  
305 310 315

Tyr His Pro Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu  
320 325 330

Gly Leu Pro Lys Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser  
335 340 345

Val Leu Glu Pro Gly Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys  
350 355 360

Gly Arg Val Pro Pro Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly  
365 370 375

Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser  
380 385 390

Ala Glu Pro Pro Leu Thr Ala Val Arg Pro Glu Gly Ser Glu Pro  
395 400 405

Pro Gly Phe Pro Thr Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser  
410 415 420

Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly  
425 430 435

Ser Gly Gly Gly Gly Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu  
440 445 450

Pro Ser Leu Thr Cys Ser Leu Thr Pro Leu Gly Leu Ala Leu Val  
455 460 465

Leu Trp Thr Val Leu Gly Pro Cys  
470

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ccctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50

ggagaggact actcactggc atattttctga ggtatctgta gaataaccac 100

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agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200

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gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450

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 <212> PRT  
 <213> Homo sapiens

<400> 405

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			20						25					30

Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
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Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Glu	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr	Thr	Phe	Pro	Leu	Lys	Asn	Ala	Glu	Asp	Leu	Asp	Val	Gly	Gln	
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Asn	Asn	Ile	Glu	Asn	Tyr	Ile	Ile	Ser	Pro	Asn	Ser	Tyr	Phe	Arg	
				170					175					180	
Val	Leu	Thr	Arg	Lys	Arg	Ser	Asp	Gly	Arg	Lys	Tyr	Pro	Glu	Leu	
				185					190					195	
Val	Leu	Asp	Lys	Ala	Leu	Asp	Arg	Glu	Glu	Glu	Ala	Glu	Leu	Arg	
				200					205					210	
Leu	Thr	Leu	Thr	Ala	Leu	Asp	Gly	Gly	Ser	Pro	Pro	Arg	Ser	Gly	
				215					220					225	
Thr	Ala	Gln	Val	Tyr	Ile	Glu	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	
				230					235					240	
Pro	Glu	Phe	Glu	Gln	Pro	Phe	Tyr	Arg	Val	Gln	Ile	Ser	Glu	Asp	
				245					250					255	
Ser	Pro	Val	Gly	Phe	Leu	Val	Val	Lys	Val	Ser	Ala	Thr	Asp	Val	
				260					265					270	
Asp	Thr	Gly	Val	Asn	Gly	Glu	Ile	Ser	Tyr	Ser	Leu	Phe	Gln	Ala	
				275					280					285	
Ser	Glu	Glu	Ile	Gly	Lys	Thr	Phe	Lys	Ile	Asn	Pro	Leu	Thr	Gly	
				290					295					300	
Glu	Ile	Glu	Leu	Lys	Lys	Gln	Leu	Asp	Phe	Glu	Lys	Leu	Gln	Ser	
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Tyr	Glu	Val	Asn	Ile	Glu	Ala	Arg	Asp	Ala	Gly	Thr	Phe	Ser	Gly	
				320					325					330	
Lys	Cys	Thr	Val	Leu	Ile	Gln	Val	Ile	Asp	Val	Asn	Asp	His	Ala	
				335					340					345	
Pro	Glu	Val	Thr	Met	Ser	Ala	Phe	Thr	Ser	Pro	Ile	Pro	Glu	Asn	
				350					355					360	
Ala	Pro	Glu	Thr	Val	Val	Ala	Leu	Phe	Ser	Val	Ser	Asp	Leu	Asp	
				365					370					375	
Ser	Gly	Glu	Asn	Gly	Lys	Ile	Ser	Cys	Ser	Ile	Gln	Glu	Asp	Leu	
				380					385					390	
Pro	Phe	Leu	Leu	Lys	Ser	Ala	Glu	Asn	Phe	Tyr	Thr	Leu	Leu	Thr	
				395					400					405	
Glu	Arg	Pro	Leu	Asp	Arg	Glu	Ser	Arg	Ala	Glu	Tyr	Asn	Ile	Thr	
				410					415					420	
Ile	Thr	Val	Thr	Asp	Leu	Gly	Thr	Pro	Met	Leu	Ile	Thr	Gln	Leu	
				425					430					435	

Asn Met Thr Val	Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro	Ala
440		445	450
Phe Thr Gln Thr	Ser Tyr Thr Leu Phe	Val Arg Glu Asn Asn	Ser
455		460	465
Pro Ala Leu His	Ile Arg Ser Val Ser	Ala Thr Asp Arg Asp	Ser
470		475	480
Gly Thr Asn Ala	Gln Val Thr Tyr Ser	Leu Leu Pro Pro Gln	Asp
485		490	495
Pro His Leu Pro	Leu Thr Ser Leu Val	Ser Ile Asn Ala Asp	Asn
500		505	510
Gly His Leu Phe	Ala Leu Arg Ser Leu	Asp Tyr Glu Ala Leu	Gln
515		520	525
Gly Phe Gln Phe	Arg Val Gly Ala Ser	Asp His Gly Ser Pro	Ala
530		535	540
Leu Ser Ser Glu	Ala Leu Val Arg Val	Val Val Leu Asp Ala	Asn
545		550	555
Asp Asn Ser Pro	Phe Val Leu Tyr Pro	Leu Gln Asn Gly Ser	Ala
560		565	570
Pro Cys Thr Glu	Leu Val Pro Arg Ala	Ala Glu Pro Gly Tyr	Leu
575		580	585
Val Thr Lys Val	Val Ala Val Asp Gly	Asp Ser Gly Gln Asn	Ala
590		595	600
Trp Leu Ser Tyr	Gln Leu Leu Lys Ala	Thr Glu Leu Gly Leu	Phe
605		610	615
Gly Val Trp Ala	His Asn Gly Glu Val	Arg Thr Ala Arg Leu	Leu
620		625	630
Ser Glu Arg Asp	Ala Ala Lys His Arg	Leu Val Val Leu Val	Lys
635		640	645
Asp Asn Gly Glu	Pro Pro Arg Ser Ala	Thr Ala Thr Leu His	Val
650		655	660
Leu Leu Val Asp	Gly Phe Ser Gln Pro	Tyr Leu Pro Leu Pro	Glu
665		670	675
Ala Ala Pro Thr	Gln Ala Gln Ala Asp	Leu Leu Thr Val Tyr	Leu
680		685	690
Val Val Ala Leu	Ala Ser Val Ser Ser	Leu Phe Leu Phe Ser	Val
695		700	705
Leu Leu Phe Val	Ala Val Arg Leu Cys	Arg Arg Ser Arg Ala	Ala
710		715	720



Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His  
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln  
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys  
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly  
770 775 780

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Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

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<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgtca ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgtct cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

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cggtcgacga ccgccccgcg tcatgcggt cctcggtgg tggcaagtat 150  
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<211> 360  
<212> PRT  
<213> Homo sapiens

<400> 410

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				20					25					30
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu
				35					40					45
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly
				50					55					60
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala
				65					70					75
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His
				80					85					90
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val
				95					100					105
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu
				110					115					120
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly
				125					130					135
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu
				140					145					150
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn
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Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg
				170					175					180
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met
				185					190					195
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys
				200					205					210
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser
				215					220					225
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu
				230					235					240
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr
				245					250					255
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly

260					265					270				
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu
				275					280					285
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys
				290					295					300
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro
				305					310					315
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu
				320					325					330
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

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<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgg cctgg 25

<210> 413

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<212> DNA

<213> Artificial Sequence

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<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150  
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<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

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Pro Asp Phe Ser Tyr	Lys Arg Ser Asn Cys	Lys Pro Ile Pro Val	
35	40	45	
Asn Leu Gln Leu Cys	His Gly Ile Glu Tyr	Gln Asn Met Arg Leu	
50	55	60	
Pro Asn Leu Leu Gly	His Glu Thr Met Lys	Glu Val Leu Glu Gln	
65	70	75	
Ala Gly Ala Trp Ile	Pro Leu Val Met Lys	Gln Cys His Pro Asp	
80	85	90	
Thr Lys Lys Phe Leu	Cys Ser Leu Phe Ala	Pro Val Cys Leu Asp	
95	100	105	
Asp Leu Asp Glu Thr	Ile Gln Pro Cys His	Ser Leu Cys Val Gln	
110	115	120	
Val Lys Asp Arg Cys	Ala Pro Val Met Ser	Ala Phe Gly Phe Pro	
125	130	135	
Trp Pro Asp Met Leu	Glu Cys Asp Arg Phe	Pro Gln Asp Asn Asp	
140	145	150	
Leu Cys Ile Pro Leu	Ala Ser Ser Asp His	Leu Leu Pro Ala Thr	
155	160	165	
Glu Glu Ala Pro Lys	Val Cys Glu Ala Cys	Lys Asn Lys Asn Asp	
170	175	180	
Asp Asp Asn Asp Ile	Met Glu Thr Leu Cys	Lys Asn Asp Phe Ala	
185	190	195	
Leu Lys Ile Lys Val	Lys Glu Ile Thr Tyr	Ile Asn Arg Asp Thr	
200	205	210	
Lys Ile Ile Leu Glu	Thr Lys Ser Lys Thr	Ile Tyr Lys Leu Asn	
215	220	225	
Gly Val Ser Glu Arg	Asp Leu Lys Lys Ser	Val Leu Trp Leu Lys	
230	235	240	
Asp Ser Leu Gln Cys	Thr Cys Glu Glu Met	Asn Asp Ile Asn Ala	
245	250	255	
Pro Tyr Leu Val Met	Gly Gln Lys Gln Gly	Gly Glu Leu Val Ile	
260	265	270	
Thr Ser Val Lys Arg	Trp Gln Lys Gly Gln	Arg Glu Phe Lys Arg	
275	280	285	
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 <213> Artificial Sequence

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 <212> DNA  
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<400> 417  
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<210> 418  
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 <212> DNA  
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<220>  
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<400> 418  
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<210> 419  
 <211> 1830  
 <212> DNA  
 <213> Homo sapiens

<400> 419  
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 cgctgggtgt tcctgtctgc gatcagcctg ctcaactgct ccaacgccac 150  
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 <212> PRT  
 <213> Homo sapiens

<400> 420

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Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45

Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60

Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
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Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90

Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105

Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val
				110					115					120

Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu
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Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu
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Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met
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Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val
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Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Glu	Asp	Ile	Pro	Leu	Met
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Leu	Gly	Val	Tyr	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser
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Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala
				215					220					225

Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys
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Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys
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Leu Gly Gly Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu  
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Glu Gln Ile Leu Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly  
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Leu Cys Gly Ala Leu Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu  
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Ala Leu Gly Pro Tyr Val Asp Arg Thr Lys His Phe Thr Glu Ala  
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Thr Lys Ile Gly Leu Cys Leu Phe Ser Leu Ala Cys Val Pro Phe  
320 325 330

Ala Leu Val Ser Gln Leu Gln Gly Gln Thr Leu Ala Leu Ala Ala  
335 340 345

Thr Cys Ser Leu Leu Gly Leu Phe Gly Phe Ser Val Gly Pro Val  
350 355 360

Ala Met Glu Leu Ala Val Glu Cys Ser Phe Pro Val Gly Glu Gly  
365 370 375

Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln Ala Glu Gly Ile  
380 385 390

Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg Arg Ser Glu  
395 400 405

Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
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Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

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Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
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Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
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Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
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<400> 421  
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 <212> PRT  
 <213> Homo sapiens

<400> 425  
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Thr Val Lys Tyr	Gln Val Ser Glu Glu Val	Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu	Ser Gln Glu Leu Gly Arg	Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala	Ala Phe Gln Val Leu Gln	Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val	Asp Ser Glu Glu Gly Leu	Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg	Glu Gln Leu Cys Arg Gln	Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp	Val Leu Ala Thr Gly Asp	Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln	Val Leu Asp Ile Asn Asp	His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu	Gln Glu Leu Glu Ile Ser	Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile	Pro Leu Asp Arg Ala Leu	Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu	His Thr Tyr Thr Leu Ser	Pro Ser Glu His Phe	170	175	180

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Ala Leu Asp Val	Ile Val Gly Pro Asp Glu	Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val	Lys Glu Leu Asp Arg Glu	Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn Gly	Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu	Val Lys Val Asn Val Leu	Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu Ala	Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile Lys	Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val Glu	Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro	Glu Val Leu Asp Thr Phe	Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val Ile Leu Arg Arg Pro Leu Asp Tyr Glu Lys Asn  
305 310 315

Pro Ala Tyr Glu Val Asp Val Gln Ala Arg Asp Leu Gly Pro Asn  
320 325 330

Pro Ile Pro Ala His Cys Lys Val Leu Ile Lys Val Leu Asp Val  
335 340 345

Asn Asp Asn Ile Pro Ser Ile His Val Thr Trp Ala Ser Gln Pro  
350 355 360

Ser Leu Val Ser Glu Ala Leu Pro Lys Asp Ser Phe Ile Ala Leu  
365 370 375

Val Met Ala Asp Asp Leu Asp Ser Gly His Asn Gly Leu Val His  
380 385 390

Cys Trp Leu Ser Gln Glu Leu Gly His Phe Arg Leu Lys Arg Thr  
395 400 405

Asn Gly Asn Thr Tyr Met Leu Leu Thr Asn Ala Thr Leu Asp Arg  
410 415 420

Glu Gln Trp Pro Lys Tyr Thr Leu Thr Leu Leu Ala Gln Asp Gln  
425 430 435

Gly Leu Gln Pro Leu Ser Ala Lys Lys Gln Leu Ser Ile Gln Ile  
440 445 450

Ser Asp Ile Asn Asp Asn Ala Pro Val Phe Glu Lys Ser Arg Tyr  
455 460 465

Glu Val Ser Thr Arg Glu Asn Asn Leu Pro Ser Leu His Leu Ile  
470 475 480

Thr Ile Lys Ala His Asp Ala Asp Leu Gly Ile Asn Gly Lys Val  
485 490 495

Ser Tyr Arg Ile Gln Asp Ser Pro Val Ala His Leu Val Ala Ile  
500 505 510

Asp Ser Asn Thr Gly Glu Val Thr Ala Gln Arg Ser Leu Asn Tyr  
515 520 525

Glu Glu Met Ala Gly Phe Glu Phe Gln Val Ile Ala Glu Asp Ser  
530 535 540

Gly Gln Pro Met Leu Ala Ser Ser Val Ser Val Trp Val Ser Leu  
545 550 555

Leu Asp Ala Asn Asp Asn Ala Pro Glu Val Val Gln Pro Val Leu  
560 565 570

Ser Asp Gly Lys Ala Ser Leu Ser Val Leu Val Asn Ala Ser Thr  
575 580 585



Gly His Leu Leu Val	Pro Ile Glu Thr	Pro Asn Gly Leu Gly	Pro
590		595	600
Ala Gly Thr Asp Thr	Pro Pro Leu Ala	Thr His Ser Ser Arg	Pro
605		610	615
Phe Leu Leu Thr Thr	Ile Val Ala Arg	Asp Ala Asp Ser Gly	Ala
620		625	630
Asn Gly Glu Pro Leu	Tyr Ser Ile Arg	Asn Gly Asn Glu Ala	His
635		640	645
Leu Phe Ile Leu Asn	Pro His Thr Gly	Gln Leu Phe Val Asn	Val
650		655	660
Thr Asn Ala Ser Ser	Leu Ile Gly Ser	Glu Trp Glu Leu Glu	Ile
665		670	675
Val Val Glu Asp Gln	Gly Ser Pro Pro	Leu Gln Thr Arg Ala	Leu
680		685	690
Leu Arg Val Met Phe	Val Thr Ser Val	Asp His Leu Arg Asp	Ser
695		700	705
Ala Arg Lys Pro Gly	Ala Leu Ser Met	Ser Met Leu Thr Val	Ile
710		715	720
Cys Leu Ala Val Leu	Leu Gly Ile Phe	Gly Leu Ile Leu Ala	Leu
725		730	735
Phe Met Ser Ile Cys	Arg Thr Glu Lys	Lys Asp Asn Arg Ala	Tyr
740		745	750

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Asn Cys Arg Glu Ala	Glu Ser Thr Tyr	Arg Gln Gln Pro Lys	Arg
755		760	765
Pro Gln Lys His Ile	Gln Lys Ala Asp	Ile His Leu Val Pro	Val
770		775	780
Leu Arg Gly Gln Ala	Gly Glu Pro Cys	Glu Val Gly Gln Ser	His
785		790	795
Lys Asp Val Asp Lys	Glu Ala Met Met	Glu Ala Gly Trp Asp	Pro
800		805	810
Cys Leu Gln Ala Pro	Phe His Leu Thr	Pro Thr Leu Tyr Arg	Thr
815		820	825
Leu Arg Asn Gln Gly	Asn Gln Gly Ala	Pro Ala Glu Ser Arg	Glu
830		835	840
Val Leu Gln Asp Thr	Val Asn Leu Leu	Phe Asn His Pro Arg	Gln
845		850	855
Arg Asn Ala Ser Arg	Glu Asn Leu Asn	Leu Pro Glu Pro Gln	Pro
860		865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

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<212> DNA

<213> Artificial Sequence

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<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

tggacacctt cagtattgat gccaaagacag gccaggtcat tctgcgtcga 50

<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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 Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
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 Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
 65 70 75  
 Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
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 Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
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 His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
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 Met Tyr Phe Phe Trp Lys Leu Gly Asp Pro Phe Pro Ile Leu Ser  
 125 130 135  
 Pro Lys His Gly Ile Leu Ser Ile Glu Gln Leu Ile Ser Arg Val  
 140 145 150  
 Gly Val Ile Gly Val Thr Leu Met Ala Leu Leu Ser Gly Phe Gly  
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 Ala Val Asn Cys Pro Tyr Thr Tyr Met Ser Tyr Phe Leu Arg Asn  
 170 175 180  
 Val Thr Asp Thr Asp Ile Leu Ala Leu Glu Arg Arg Leu Leu Gln

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Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
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Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
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Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
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Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
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	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
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Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Arg Thr Ile	Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
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<223> unknown base

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<212> DNA  
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<223> Synthetic oligonucleotide probe

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<210> 434

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<223> Synthetic oligonucleotide probe

<400> 434

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 435

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<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

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 a 3951

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 <211> 1141  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Gly Glu Pro Gly Ser Leu Phe Gly Phe Ser Val Ala Leu His Arg  
 50 55 60  
 Gln Leu Gln Pro Arg Pro Gln Ser Trp Leu Leu Val Gly Ala Pro  
 65 70 75  
 Gln Ala Leu Ala Leu Pro Gly Gln Gln Ala Asn Arg Thr Gly Gly  
 80 85 90  
 Leu Phe Ala Cys Pro Leu Ser Leu Glu Glu Thr Asp Cys Tyr Arg  
 95 100 105

Val Asp Ile Asp	Gln Gly Ala Asp	Met Gln Lys Glu Ser Lys	Glu
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Asn Gln Trp Leu	Gly Val Ser Val Arg	Ser Gln Gly Pro Gly	Gly
125		130	135
Lys Ile Val Thr	Cys Ala His Arg Tyr	Glu Ala Arg Gln Arg	Val
140		145	150
Asp Gln Ile Leu	Glu Thr Arg Asp Met	Ile Gly Arg Cys Phe	Val
155		160	165
Leu Ser Gln Asp	Leu Ala Ile Arg Asp	Glu Leu Asp Gly Gly	Glu
170		175	180
Trp Lys Phe Cys	Glu Gly Arg Pro Gln	Gly His Glu Gln Phe	Gly
185		190	195
Phe Cys Gln Gln	Gly Thr Ala Ala Ala	Phe Ser Pro Asp Ser	His
200		205	210
Tyr Leu Leu Phe	Gly Ala Pro Gly Thr	Tyr Asn Trp Lys Gly	Thr
215		220	225
Ala Arg Val Glu	Leu Cys Ala Gln Gly	Ser Ala Asp Leu Ala	His
230		235	240
Leu Asp Asp Gly	Pro Tyr Glu Ala Gly	Gly Glu Lys Glu Gln	Asp
245		250	255
Pro Arg Leu Ile	Pro Val Pro Ala Asn	Ser Tyr Phe Gly Phe	Ser
260		265	270
<del>Ile Asp Ser Gly</del>	<del>Lys Gly Leu Val Arg</del>	<del>Ala Glu Glu Leu Ser</del>	<del>Phe</del>
<del>275</del>		<del>280</del>	<del>285</del>
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Leu Arg Lys Asp	Ser Ala Ser Arg Leu	Val Pro Glu Val Met	Leu
305		310	315
Ser Gly Glu Arg	Leu Thr Ser Gly Phe	Gly Tyr Ser Leu Ala	Val
320		325	330
Ala Asp Leu Asn	Ser Asp Gly Trp Pro	Asp Leu Ile Val Gly	Ala
335		340	345
Pro Tyr Phe Phe	Glu Arg Gln Glu Glu	Leu Gly Gly Ala Val	Tyr
350		355	360
Val Tyr Leu Asn	Gln Gly Gly His Trp	Ala Gly Ile Ser Pro	Leu
365		370	375
Arg Leu Cys Gly	Ser Pro Asp Ser Met	Phe Gly Ile Ser Leu	Ala
380		385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly	Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys	Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro	Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly	Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro	Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg	Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro	Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser	Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro	Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala	Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe	Leu Ser Arg Asn Leu Glu	545	550	555
<del>Glu Pro Lys His</del>	<del>Gln Ala Ser Gly Thr</del>	<del>Val Trp Leu Lys His Gln</del>	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met	Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val	Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln	Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala	His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln	Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val	His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro	Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly
680		685 690
Leu Glu Leu Met Val	Thr Asn Leu Pro Ser Asp Pro Ala Gln Pro	
695		700 705
Gln Ala Asp Gly Asp	Asp Ala His Glu Ala Gln Leu Leu Val Met	
710		715 720
Leu Pro Asp Ser Leu	His Tyr Ser Gly Val Arg Ala Leu Asp Pro	
725		730 735
Ala Glu Lys Pro Leu	Cys Leu Ser Asn Glu Asn Ala Ser His Val	
740		745 750
Glu Cys Glu Leu Gly	Asn Pro Met Lys Arg Gly Ala Gln Val Thr	
755		760 765
Phe Tyr Leu Ile Leu	Ser Thr Ser Gly Ile Ser Ile Glu Thr Thr	
770		775 780
Glu Leu Glu Val Glu	Leu Leu Leu Ala Thr Ile Ser Glu Gln Glu	
785		790 795
Leu His Pro Val Ser	Ala Arg Ala Arg Val Phe Ile Glu Leu Pro	
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Leu Ser Ile Ala Gly	Met Ala Ile Pro Gln Gln Leu Phe Phe Ser	
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Glu Leu Glu Gly Gly	Gln Gly Pro Gly Gln Lys Gly Leu Cys Ser	
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Pro Arg Pro Asn Ile	Leu His Leu Asp Val Asp Ser Arg Asp Arg	
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Arg Gln Glu Pro Ser	Met Ser Trp Trp Pro Val Ser Ser Ala Glu	
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Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catcctccat gtctcccatg aggtctctat tgctccaaga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

cgcgccgggc gcagggagct gaggggacgg ctcgagacgg cggcgcgctgc 50

agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100

ggagctgcga gcacagtgcg ggctcacaac aagatgctca aggtgtcagc 150

cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200

ccgcggcggt ggctgcagcc gggggcggt cggacggcgg taattttctg 250

gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300

acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350

ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400

tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450

tcagactgca gtctgcatta gtcaccggag gttacacac aggatgaaag 500

aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550

aagcagtgcc cagtggctta tcccagccct gtttgtggtt cagatggtca 600

tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650

aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700

cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750

caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800

gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850

agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900



gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950  
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 aattcttgtg acacatacaa ggacagttta atatctaata atgagtgggtg 1050  
 ctactgcttc cagagacagc aagaccacc ttgccagact gagctcagca 1100  
 atattcagaa gcggcaaggg gtaaagaagc tcctaggaca gtatatcccc 1150  
 ctgtgtgatg aagatggtta ctacaagcca acacaatgtc atggcagtgt 1200  
 tggacagtgc tgggtgtgtg acagatatgg aatgaagtc atgggatcca 1250  
 gaataaatgg tgttcagat tgtgctatag attttgagat ctccggagat 1300  
 tttgctagtg gcgattttca tgaatggact gatgatgagg atgatgaaga 1350  
 cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400  
 gggatgatga tgatgggtgg gatgaccatg atgtatacat ttgattgatg 1450  
 acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500  
 cctattttaa attatcttct tcccaataa caaatgatt ctaaacctca 1550  
 catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600  
 ttatgtttaa ataagaatca tttgctttga gtttttatat tccttacaca 1650  
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 ctactataat aaatttttca cgagaacaaa ctttgtaaatt cttccataag 1750

caaatgaca gctagtgtt gggatcgtac atgttaattt tttgaaagat 1800  
 aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850  
 aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
 ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
 aaaaaaaaaa aaaa 1964

<210> 442  
 <211> 436  
 <212> PRT  
 <213> Homo sapiens

<400> 442  
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 20 25 30  
 Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65					70					75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80					85					90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95					100					105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110					115					120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125					130					135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140					145					150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
				155					160					165					
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170					175					180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
				185					190					195					
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200					205					210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215					220					225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230					235					240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245					250					255					
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln					
				260					265					270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275					280					285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
				290					295					300					
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305					310					315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

320	325	330
Lys Lys Leu Leu Gly Gln Tyr Ile Pro	Leu Cys Asp Glu Asp Gly	
335	340	345
Tyr Tyr Lys Pro Thr Gln Cys His Gly	Ser Val Gly Gln Cys Trp	
350	355	360
Cys Val Asp Arg Tyr Gly Asn Glu Val	Met Gly Ser Arg Ile Asn	
365	370	375
Gly Val Ala Asp Cys Ala Ile Asp Phe	Glu Ile Ser Gly Asp Phe	
380	385	390
Ala Ser Gly Asp Phe His Glu Trp Thr	Asp Asp Glu Asp Asp Glu	
395	400	405
Asp Asp Ile Met Asn Asp Glu Asp Glu	Ile Glu Asp Asp Asp Glu	
410	415	420
Asp Glu Gly Asp Asp Asp Asp Gly Gly	Asp Asp His Asp Val Tyr	
425	430	435

Ile

<210> 443  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

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<400> 443  
 cagcaatatt cagaagcggc aaggg 25

<210> 444  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 444  
 catcatggtc atcaccacca tcatcatc 28

<210> 445  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 445

ggttactaca agccaacaca atgtcatggc agtggttgac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100

cagggatggg cgacaagatc tggctgccct tccccgtgct ctttctggcc 150

gctctgcctc cgggtgctgct gcctggggcg gccgggttca caccttcct 200

cgatagcgac ttcaccttta cccttcccgc cggccagaag gagtgcttct 250

accagcccat gccctgaag gcctcgctgg agatcgagta ccaagtttta 300

gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350

aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400

ctgaagttgg tgattacatg ttctgctttg acaatacatt cagcaccatt 450

tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500

ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550

tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600

agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650

tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700

ctatgggtaa tttagtggtc atggtgggtg tgtcagccat tcaagtttat 750

atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaaactc 800

caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850

tgttacagtc aagaccatta atggtcttct ccaaaatatt ttgagatata 900

aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950

tgtgcaagta atcctgctga tccagttgta ctttaagtgtg taacaggaat 1000

attttgcaga atataggttt aactgaatga agccatatta ataactgcat 1050

tttcctaact ttgaaaaatt ttgcaaagt cttaggtgat ttaaataaat 1100

gagtattggg cctaattgca acaccagtct gtttttaaca gggttctatta 1150

cccagaactt ttttgtaaat gcggcagtta caaattaact gtggaagttt 1200

tcagttttta gttataaatc acctgagaat tacctaataa tggattgaat 1250

aaatcttttag actacaaaag cccaactttt ctctatttac atatgcatct 1300  
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350  
agatttttat aaccaaatac atttcagtgt aacatattag cagaaagcat 1400  
tagtctttgt actttgctta cattcccaa agctgacatt ttcacgattc 1450  
ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500  
aatgaagaa tatagttaa aagcttcctc ctccataggg acacattttc 1550  
tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600  
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agaatttaga aaaacttgag aaaacctaat ccaaaataaa attcacttaa 1850  
gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
tactcataac ataaatcaaa ggagatgatt aatttcagt tagctggaag 1950  
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agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100  
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gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacctatata 2200  
tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250  
tcaagtacta gtaatttaac ttcattcatga atgaactata atttttaagt 2300  
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cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
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 taccatataa aaacgataat tgctttattt ggaaaagaat ttaggaatac 2950  
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 cataacccaaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatat 3050  
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100  
 tccatttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150  
 aacagctcat tttgtctttt tcaatatata aatttttaaaa atactacaat 3200  
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250  
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 aaaaaatgag cacttacaat tgtatgtctc ctcaaatgaa gattctttat 3450  
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcattctgaa 3500  
 gtacaataat gcacaatcag tgttgcctaa actgctttat acttataaac 3550  
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 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val	Leu Asp Gly Ala Gly	Leu Asp Ile Asp Phe His
	65	70 75
Leu Ala Ser Pro	Glu Gly Lys Thr Leu Val	Phe Glu Gln Arg Lys
	80	85 90
Ser Asp Gly Val	His Thr Val Glu Thr	Glu Val Gly Asp Tyr Met
	95	100 105
Phe Cys Phe Asp	Asn Thr Phe Ser Thr	Ile Ser Glu Lys Val Ile
	110	115 120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln Glu
	125	130 135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu Asp
	140	145 150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys Ser
	155	160 165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala Phe
	170	175 180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg Val
	185	190 195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val Ser
	200	205 210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys Arg
	215	220 225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

cccagcaggg ctgggcgaca aga 23

<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

gtcttccagt ttcatatcca ata 23

<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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agcataccag atctcaccag agagtcgcag acactatgct gcctcccatg 100

gccctgccca gtgtgtcctg gatgctgctt tcttgctca ttctcctgtg 150

tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200

gctgtcccaa aggctccaag gcctatggct cccctgcta tgccttgttt 250

ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300

ctctggaaaa ctggtgtctg tgctcagtgg ggctgaggga tccttcgtgt 350

~~cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400~~

ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450

gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500

ccatcttaaa ccttgccac tgtgggagcc tgtcaagaag cacaggattt 550

ctgaagtgga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600

gttcaaggac tagggcaggt gggaagtcag cagcctcagc ttggcgtgca 650

gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700

ttctcccaa actgccctac ctgactacct tgtcatgac ctccttcttt 750

ttcctttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800

gagatctcag agaataataa taaaaatggt actttataaa aaaaaaaaaa 850

aaaaaaaaa 859

<210> 452

<211> 175



<212> PRT  
<213> Homo sapiens

<400> 452

Met	Leu	Pro	Pro	Met	Ala	Leu	Pro	Ser	Val	Ser	Trp	Met	Leu	Leu
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Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln
			20						25					30
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys
			35						40					45
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser
			50						55					60
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys
			65						70					75
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser
			80						85					90
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly
			95						100					105
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp
			110						115					120
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys
			125						130					135
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser
			140						145					150

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Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala
			155						160					165

Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp
			170						175

<210> 453  
<211> 550  
<212> DNA  
<213> Homo sapiens

<400> 453

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tggggtgaga gcacagagga gtgggcccgg accatgcggg ggacgcggct 100  
ggcgctcctg gcgctggtgc tggctgcctg cggagagctg gcgccggccc 150  
tgcgctgcta cgtctgtccg gagcccacag gagtgtcga ctgtgtcacc 200  
atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400  
 tctgaacagc ctccactgcg gggccctcac gtcctccca ctcttgagcc 450  
 tccgactgta gagtccccgc ccacccccat ggcctatgc ggcccagccc 500  
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaaa aaaaaaaaaa 550

<210> 454

<211> 125

<212> PRT

<213> Homo sapiens

<400> 454

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala  
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu  
 20 25 30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr  
 35 40 45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val  
 50 55 60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser  
 65 70 75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro  
 80 85 90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro  
 95 100 105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu  
 110 115 120

Leu Ser Leu Arg Leu  
 125

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

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atcttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250  
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 acccaggctc tgcagtcagc gccgcgcggg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caactaccag ccgtaccggt gcgcagagga 400  
 cgaggagtgc ggcaactgat agtactgcgc tagtcccacc cgcggagggg 450  
 acgcaggcgt gcaaactctgt ctgcctgca ggaagcgccg aaaacgctgc 500  
 atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
 tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
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 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750  
 tctggtccaa gatctgtaaa cctgtcctga aagaaggta agtgtgtacc 800  
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttgta 850  
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<210> 456

<211> 266

<212> PRT  
<213> Homo sapiens

<400> 456

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Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
35 40 45

Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
50 55 60

Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
65 70 75

Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu  
80 85 90

Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly Gly Asp  
95 100 105

Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys Arg  
110 115 120

Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn  
125 130 135

Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile  
140 145 150

Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu  
155 160 165

Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His  
170 175 180

Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys  
185 190 195

Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys  
200 205 210

Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg Arg  
215 220 225

Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly  
230 235 240

Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser  
245 250 255

Asn Ser Ser Arg Leu His Thr Cys Gln Arg His  
260 265

<210> 457  
<211> 638  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
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509, 556  
<223> unknown base

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<210> 458  
<211> 4040  
<212> DNA  
<213> Homo sapiens

<400> 458  
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<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

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			20						25				30	

Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr
			35						40				45	

Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu
			50						55				60	

Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly
			65						70				75	



Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
<del>Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala</del>	<del>245</del>	<del>250</del>	<del>255</del>
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly		380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His	Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile	Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr	Phe Asn Glu Leu Val Thr	515	520	525
<del>Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro</del>		<del>530</del>	<del>535</del>	<del>540</del>
Trp Cys His Pro Cys Gln Val Leu Met	Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn	Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln	Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys	Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg	Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln	Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu	Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe
				650					655					660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val
				665					670					675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln
				680					685					690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr
				695					700					705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg
				710					715					720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr
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Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu			
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<210> 460  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 460  
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<210> 461  
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<220>  
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<400> 461  
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<210> 462  
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<220>  
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<210> 463  
 <211> 1818  
 <212> DNA

<213> Homo sapiens

<400> 463

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caccatcatc tactcctact tggagtcggt ggtgaagttt ttcattcttc 150  
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<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
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 Arg Lys Ser Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala Gly  
 35 40 45  
 His Gly Ile Gly Arg Gln Thr Thr Tyr Glu Phe Ala Lys Arg Gln  
 50 55 60  
 Ser Ile Leu Val Leu Trp Asp Ile Asn Lys Arg Gly Val Glu Glu  
 65 70 75  
 Thr Ala Ala Glu Cys Arg Lys Leu Gly Val Thr Ala His Ala Tyr  
 80 85 90  
 Val Val Asp Cys Ser Asn Arg Glu Glu Ile Tyr Arg Ser Leu Asn  
 95 100 105  
 Gln Val Lys Lys Glu Val Gly Asp Val Thr Ile Val Val Asn Asn  
 110 115 120  
 Ala Gly Thr Val Tyr Pro Ala Asp Leu Leu Ser Thr Lys Asp Glu  
 125 130 135  
 Glu Ile Thr Lys Thr Phe Glu Val Asn Ile Leu Gly His Phe Trp  
 140 145 150  
 Ile Thr Lys Ala Leu Leu Pro Ser Met Met Glu Arg Asn His Gly

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His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro		
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
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Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
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<210> 465  
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 <212> DNA  
 <213> Homo sapiens

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<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

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Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20					25						30
Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
			35					40						45
Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50					55						60

Thr Ala Asp Ser Asp Val Asp Glu Phe Leu Asp Lys Phe Leu Ser  
65 70 75

Ala Gly Val Lys Gln Ser Asp Leu Pro Arg Lys Glu Thr Glu Gln  
80 85 90

Pro Pro Ala Pro Gly Ser Met Glu Glu Ser Val Arg Gly Tyr Asp  
95 100 105

Trp Ser Pro Arg Asp Ala Arg Arg Ser Pro Asp Gln Gly Arg Gln  
110 115 120

Gln Ala Glu Arg Arg Ser Val Leu Arg Gly Phe Cys Ala Asn Ser  
125 130 135

Ser Leu Ala Phe Pro Thr Lys Glu Arg Ala Phe Asp Asp Ile Pro  
140 145 150

Asn Ser Glu Leu Ser His Leu Ile Val Asp Asp Arg His Gly Ala  
155 160 165

Ile Tyr Cys Tyr Val Pro Lys Val Ala Cys Thr Asn Trp Lys Arg  
170 175 180

Val Met Ile Val Leu Ser Gly Ser Leu Leu His Arg Gly Ala Pro  
185 190 195

Tyr Arg Asp Pro Leu Arg Ile Pro Arg Glu His Val His Asn Ala  
200 205 210

Ser Ala His Leu Thr Phe Asn Lys Phe Trp Arg Arg Tyr Gly Lys  
215 220 225

Leu Ser Arg His Leu Met Lys Val Lys Leu Lys Lys Tyr Thr Lys  
230 235 240

Phe Leu Phe Val Arg Asp Pro Phe Val Arg Leu Ile Ser Ala Phe  
245 250 255

Arg Ser Lys Phe Glu Leu Glu Asn Glu Glu Phe Tyr Arg Lys Phe  
260 265 270

Ala Val Pro Met Leu Arg Leu Tyr Ala Asn His Thr Ser Leu Pro  
275 280 285

Ala Ser Ala Arg Glu Ala Phe Arg Ala Gly Leu Lys Val Ser Phe  
290 295 300

Ala Asn Phe Ile Gln Tyr Leu Leu Asp Pro His Thr Glu Lys Leu  
305 310 315

Ala Pro Phe Asn Glu His Trp Arg Gln Val Tyr Arg Leu Cys His  
320 325 330

Pro Cys Gln Ile Asp Tyr Asp Phe Val Gly Lys Leu Glu Thr Leu  
335 340 345



Asp Glu Asp Ala Ala Gln Leu Leu Gln Leu Leu Gln Val Asp Arg  
350 355 360

Gln Leu Arg Phe Pro Pro Ser Tyr Arg Asn Arg Thr Ala Ser Ser  
365 370 375

Trp Glu Glu Asp Trp Phe Ala Lys Ile Pro Leu Ala Trp Arg Gln  
380 385 390

Gln Leu Tyr Lys Leu Tyr Glu Ala Asp Phe Val Leu Phe Gly Tyr  
395 400 405

Pro Lys Pro Glu Asn Leu Leu Arg Asp  
410

<210> 467

<211> 1071

<212> DNA

<213> Homo sapiens

<400> 467

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gggggcgggc ggggcatcgg agctgggacg gtgcgcgcct tcgtgaacag 200

cgggggccga gtggttatct gcgacaagga tgagtctggg ggccgggccc 250

tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300

gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350

cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400

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tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750

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ccataaaaac gatttgcagc c 1071

<210> 468  
<211> 270  
<212> PRT  
<213> Homo sapiens

<400> 468

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Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly	35	40	45	
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu	50	55	60	
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu	65	70	75	
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala	80	85	90	
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln	95	100	105	
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr	110	115	120	
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn	125	130	135	
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln	140	145	150	
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr	155	160	165	
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn	170	175	180	
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu	185	190	195	
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met	200	205	210	

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
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<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

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 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaag tgtgaggtca 300  
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 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400

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gtgccttgtt ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
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 gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
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 ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 470  
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 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
                   20                  25                  30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val
				35					40					45
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu
				50					55					60
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn
				65					70					75
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu
				80					85					90
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile
				95					100					105
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg
				110					115					120
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp
				125					130					135
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg
				140					145					150
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln
				155					160					165
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe
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<210> 471

<211> 2368

<212> DNA

<213> Homo sapiens

<400> 471

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cggcccgcag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200

cgacggcagg ccccaggag gccgcgctgc cgccggagca gagccgggtc 250

cagcccatga ccgcctccaa ctggacgctg gtgatggagg gcgagtggat 300

gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350

aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400

aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450

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<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

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Ala	Trp	Ile	Ala	Ala	Val	Ala	Ala	Thr	Ala	Gly	Pro	Glu	Glu	Ala
			20						25					30

Ala	Leu	Pro	Pro	Glu	Gln	Ser	Arg	Val	Gln	Pro	Met	Thr	Ala	Ser
				35					40					45

Asn	Trp	Thr	Leu	Val	Met	Glu	Gly	Glu	Trp	Met	Leu	Lys	Phe	Tyr
				50					55					60

Ala	Pro	Trp	Cys	Pro	Ser	Cys	Gln	Gln	Thr	Asp	Ser	Glu	Trp	Glu
				65					70					75

Ala	Phe	Ala	Lys	Asn	Gly	Glu	Ile	Leu	Gln	Ile	Ser	Val	Gly	Lys
				80					85					90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105

Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120

Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135

Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150

Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr	170	175	180
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala	185	190	195
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile	200	205	210
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg	215	220	225
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln	230	235	240
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu	245	250	255
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu	260	265	270
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu	275	280	285
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly	290	295	300
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu	305	310	315
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr	320	325	330

Glu Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala	335	340	345
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Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

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<210> 474

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctcctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

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<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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<210> 477  
 <211> 201  
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 <213> Homo sapiens

<400> 477

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Val	Ser	Glu	Lys	Gly	Ser	Cys	Ala	Ala	Ser	Pro	Pro	Trp	Arg	Leu	35	40	45	
Ile	Ala	Val	Ile	Leu	Gly	Ile	Leu	Cys	Leu	Val	Ile	Leu	Val	Ile	50	55	60	
Ala	Val	Val	Leu	Gly	Thr	Met	Gly	Val	Leu	Ser	Ser	Pro	Cys	Pro	65	70	75	
Pro	Asn	Trp	Ile	Ile	Tyr	Glu	Lys	Ser	Cys	Tyr	Leu	Phe	Ser	Met	80	85	90	
Ser	Leu	Asn	Ser	Trp	Asp	Gly	Ser	Lys	Arg	Gln	Cys	Trp	Gln	Leu	95	100	105	
Gly	Ser	Asn	Leu	Leu	Lys	Ile	Asp	Ser	Ser	Asn	Glu	Leu	Gly	Phe	110	115	120	
Ile	Val	Lys	Gln	Val	Ser	Ser	Gln	Pro	Asp	Asn	Ser	Phe	Trp	Ile	125	130	135	
Gly	Leu	Ser	Arg	Pro	Gln	Thr	Glu	Val	Pro	Trp	Leu	Trp	Glu	Asp	140	145	150	
Gly	Ser	Thr	Phe	Ser	Ser	Asn	Leu	Phe	Gln	Ile	Arg	Thr	Thr	Ala	155	160	165	
Thr	Gln	Glu	Asn	Pro	Ser	Pro	Asn	Cys	Val	Trp	Ile	His	Val	Ser	170	175	180	
Val	Ile	Tyr	Asp	Gln	Leu	Cys	Ser	Val	Pro	Ser	Tyr	Ser	Ile	Cys	185	190	195	
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<223> Synthetic oligonucleotide probe

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<220>  
<223> Synthetic oligonucleotide probe

<400> 479  
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<220>  
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<400> 480  
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<210> 481  
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<212> DNA  
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<220>  
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<210> 482  
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<213> Homo sapiens

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 <212> PRT  
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<400> 483  
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 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75  
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe  
 80 85 90

Cys Leu Tyr Trp Asn Arg His Ala Gly Arg Leu His Leu Leu Tyr  
95 100 105

Gly Lys Arg Asp Phe Leu Leu Ser Asp Lys Ala Ser Ser Leu Leu  
110 115 120

Cys Phe Gln His Gln Glu Glu Ser Leu Ala Gln Gly Pro Pro Leu  
125 130 135

Leu Ala Thr Ser Val Thr Ser Trp Trp Ser Pro Gln Asn Ile Ser  
140 145 150

Leu Pro Ser Ala Ala Ser Phe Thr Phe Ser Phe His Ser Pro Pro  
155 160 165

His Thr Ala Ala His Asn Ala Ser Val Asp Met Cys Glu Leu Lys  
170 175 180

Arg Asp Leu Gln Leu Leu Ser Gln Phe Leu Lys His Pro Gln Lys  
185 190 195

Ala Ser Arg Arg Pro Ser Ala Ala Pro Ala Ser Gln Gln Leu Gln  
200 205 210

Ser Leu Glu Ser Lys Leu Thr Ser Val Arg Phe Met Gly Asp Met  
215 220 225

Val Ser Phe Glu Glu Asp Arg Ile Asn Ala Thr Val Trp Lys Leu  
230 235 240

Gln Pro Thr Ala Gly Leu Gln Asp Leu His Ile His Ser Arg Gln  
245 250 255

Glu Glu Glu Gln Ser Glu Ile Met Glu Tyr Ser Val Leu Leu Pro  
260 265 270

Arg Thr Leu Phe Gln Arg Thr Lys Gly Arg Ser Gly Glu Ala Glu  
275 280 285

Lys Arg Leu Leu Leu Val Asp Phe Ser Ser Gln Ala Leu Phe Gln  
290 295 300

Asp Lys Asn Ser Ser Gln Val Leu Gly Glu Lys Val Leu Gly Ile  
305 310 315

Val Val Gln Asn Thr Lys Val Ala Asn Leu Thr Glu Pro Val Val  
320 325 330

Leu Thr Phe Gln His Gln Leu Gln Pro Lys Asn Val Thr Leu Gln  
335 340 345

Cys Val Phe Trp Val Glu Asp Pro Thr Leu Ser Ser Pro Gly His  
350 355 360

Trp Ser Ser Ala Gly Cys Glu Thr Val Arg Arg Glu Thr Gln Thr  
365 370 375

Ser Cys Phe Cys Asn His Leu Thr Tyr Phe Ala Val Leu Met Val  
380 385 390

Ser Ser Val Glu Val Asp Ala Val His Lys His Tyr Leu Ser Leu  
395 400 405

Leu Ser Tyr Val Gly Cys Val Val Ser Ala Leu Ala Cys Leu Val  
410 415 420

Thr Ile Ala Ala Tyr Leu Cys Ser Arg Val Pro Leu Pro Cys Arg  
425 430 435

Arg Lys Pro Arg Asp Tyr Thr Ile Lys Val His Met Asn Leu Leu  
440 445 450

Leu Ala Val Phe Leu Leu Asp Thr Ser Phe Leu Leu Ser Glu Pro  
455 460 465

Val Ala Leu Thr Gly Ser Glu Ala Gly Cys Arg Ala Ser Ala Ile  
470 475 480

Phe Leu His Phe Ser Leu Leu Thr Cys Leu Ser Trp Met Gly Leu  
485 490 495

Glu Gly Tyr Asn Leu Tyr Arg Leu Val Val Glu Val Phe Gly Thr  
500 505 510

Tyr Val Pro Gly Tyr Leu Leu Lys Leu Ser Ala Met Gly Trp Gly  
515 520 525

Phe Pro Ile Phe Leu Val Thr Leu Val Ala Leu Val Asp Val Asp  
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Asn Tyr Gly Pro Ile Ile Leu Ala Val His Arg Thr Pro Glu Gly  
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Val Ile Tyr Pro Ser Met Cys Trp Ile Arg Asp Ser Leu Val Ser  
560 565 570

Tyr Ile Thr Asn Leu Gly Leu Phe Ser Leu Val Phe Leu Phe Asn  
575 580 585

Met Ala Met Leu Ala Thr Met Val Val Gln Ile Leu Arg Leu Arg  
590 595 600

Pro His Thr Gln Lys Trp Ser His Val Leu Thr Leu Leu Gly Leu  
605 610 615

Ser Leu Val Leu Gly Leu Pro Trp Ala Leu Ile Phe Phe Ser Phe  
620 625 630

Ala Ser Gly Thr Phe Gln Leu Val Val Leu Tyr Leu Phe Ser Ile  
635 640 645

Ile Thr Ser Phe Gln Gly Phe Leu Ile Phe Ile Trp Tyr Trp Ser  
650 655 660



Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn  
665 670 675

Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser  
680 685 690

Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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<210> 485

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

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<210> 486

<211> 24

<212> DNA

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<220>

<223> Synthetic oligonucleotide probe

<400> 486

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

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<222> 2715

<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe
			20						25					30

Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45

His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60

Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75

Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
				80					85					90

Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys
				95					100					105

Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu
				110					115					120

Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135

Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150

Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180
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Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	200	205	210
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	215	220	225
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	230	235	240
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	245	250	255
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	260	265	270
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	275	280	285
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	290	295	300
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	305	310	315
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	320	325	330

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His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	335	340	345
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 Gly Gly Ile Pro Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn  
 65 70 75

His Ile Pro Asp Ile Ser Pro Ala Ser Phe His Arg Leu Asp His  
 80 85 90  
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 Gly Ser Lys Asn Asn Met Cys Ile Lys Arg Leu Gln Ile Lys Pro  
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 Gly Asn Gln Leu Leu Glu Ile Pro Gln Gly Leu Pro Pro Ser Leu  
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 Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile Phe Ser Ile Arg Lys  
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Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser  
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Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys  
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Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu  
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365 370 375

Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu  
380 385 390

Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly  
395 400 405

Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe  
410 415 420

Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro  
425 430 435

Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr  
440 445 450

Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr  
455 460 465

Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys  
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Ser	Asp	Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser
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Gly	Asn	Leu	Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro
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Leu	Ala	Glu	Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp
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Leu	Leu	His	Ser	Thr	Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val
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Leu	Asp	Ile	Ser	Ser	Asn	Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile
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Thr	His	Met	Leu	Asn	Phe	Thr	Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys
				590						595				600
Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	Ser	Ser	Ser	Thr	Ser	Arg	Thr
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Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu	Glu	Phe	Arg	Gly	Asn	His
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Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr  
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Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val  
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830 835 840

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Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile  
875 880 885

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Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln  
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Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr  
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Val Gly Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile  
65 70 75

Thr His Ile Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr  
80 85 90

Lys Ile Asn Leu Asn His Asn Pro Asn Val Gln His Gln Asn Gly  
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Asn Pro Gly Ile Gln Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala  
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Phe Leu Asn Leu Lys Asn Leu Arg Glu Leu Leu Leu Glu Asp Asn  
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Gln Leu Pro Gln Ile Pro Ser Gly Leu Pro Glu Ser Leu Thr Glu  
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Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn Ile Thr Lys Glu Gly  
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Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr Leu Ala Trp Asn  
170 175 180

Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile Glu Asp Gly  
185 190 195

Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu Ser Phe  
200 205 210

Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu Arg  
215 220 225

Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu  
230 235 240



Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly
				245					250					255
Asn	Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys
				260					265					270
Asp	Gly	Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn
				275					280					285
Leu	Thr	Gln	Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg
				290					295					300
Lys	Ile	Asn	Ala	Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val
				305					310					315
Leu	Asp	Leu	Glu	Phe	Asn	Tyr	Leu	Val	Gly	Glu	Ile	Val	Ser	Gly
				320					325					330
Ala	Phe	Leu	Thr	Met	Leu	Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser
				335					340					345
Phe	Asn	Tyr	Ile	Lys	Gly	Ser	Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser
				350					355					360
Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	Leu	Arg	Ala	Leu	His	Leu	Arg
				365					370					375
Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	Asp	Asp	Phe	Gln	Pro	Leu
				380					385					390
Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn	Leu	Gly	Ile	Asn	Phe
				395					400					405

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Ile	Lys	Gln	Ile	Asp	Phe	Lys	Leu	Phe	Gln	Asn	Phe	Ser	Asn	Leu
				410					415					420
Glu	Ile	Ile	Tyr	Leu	Ser	Glu	Asn	Arg	Ile	Ser	Pro	Leu	Val	Lys
				425					430					435
Asp	Thr	Arg	Gln	Ser	Tyr	Ala	Asn	Ser	Ser	Ser	Phe	Gln	Arg	His
				440					445					450
Ile	Arg	Lys	Arg	Arg	Ser	Thr	Asp	Phe	Glu	Phe	Asp	Pro	His	Ser
				455					460					465
Asn	Phe	Tyr	His	Phe	Thr	Arg	Pro	Leu	Ile	Lys	Pro	Gln	Cys	Ala
				470					475					480
Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	Leu	Asn	Ser	Ile	Phe	Phe
				485					490					495
Ile	Gly	Pro	Asn	Gln	Phe	Glu	Asn	Leu	Pro	Asp	Ile	Ala	Cys	Leu
				500					505					510
Asn	Leu	Ser	Ala	Asn	Ser	Asn	Ala	Gln	Val	Leu	Ser	Gly	Thr	Glu
				515					520					525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn  
530 535 540

Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp  
545 550 555

Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile  
560 565 570

Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn  
575 580 585

Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr  
590 595 600

Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe  
605 610 615

Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg  
620 625 630

Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp  
635 640 645

Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu  
650 655 660

Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met  
665 670 675

Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu  
680 685 690

Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp  
695 700 705

Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser  
710 715 720

His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val  
725 730 735

Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr  
740 745 750

Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser  
755 760 765

Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile  
770 775 780

Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile  
785 790 795

Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg  
800 805 810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp  
815 820 825

Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr  
830 835 840

Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp  
845 850 855

Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr  
860 865 870

Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser  
875 880 885

Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu  
890 895 900

Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu  
905 910 915

Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp  
920 925 930

Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val  
935 940 945

Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe  
950 955 960

Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile  
965 970 975

Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu  
980 985 990

Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro  
995 1000 1005

Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn  
1010 1015 1020

Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val  
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Asp Ser Ile Lys Gln Tyr  
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<210> 499

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 499  
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<210> 500  
<211> 20  
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<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 500  
atccatgagc ctctgatggg 20

<210> 501  
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<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 501  
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<210> 502  
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<220>  
<223> Synthetic oligonucleotide probe

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<400> 502  
gccgagacaa aaacgttctc c 21

<210> 503  
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<220>  
<223> Synthetic oligonucleotide probe

<400> 503  
catccatgtt ctcatccatt agcc 24

<210> 504  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 504  
tcgacaacct catgcagagc atcaaccaa gcaagaaaac agtatt 46

<210> 505  
<211> 1738  
<212> DNA  
<213> Homo sapiens

<400> 505

ccaggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50  
ctagagatcc ctcgacctcg acccacgcgt ccgccaagct ggccctgcac 100  
ggctgcaagg gaggtcctg tggacaggcc aggcagggtg gcctcaggag 150  
gtgcctccag gcggccagtg ggctgaggc cccagcaagg gctagggctc 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagccccc aggaccgggg aggcacaggt ggccccacc 300  
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cgccaggcca cccagaggag aaggccaccc cgcctggagg cacaggccat 400  
gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtgg 450  
gcggcacaga gcacgcctac cggcccggcc gtaggggtgtg tgctgtccgg 500  
gtcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550  
cttctcacc acctgcgacg ggcaccgggc ctgcagcacc taccgaacca 600  
tctataggac cgcctaccgc cgcagccctg ggctggcccc tgccaggcct 650

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cgctacgcgt gctgccccgg ctggaagagg accagcgggc ttctggggc 700  
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tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc 800  
cagtcagatg tggatgaatg cagtgtagg aggggcggct gtccccagcg 850  
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 aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1700  
 gcccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 506

Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
 1 5 10 15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30

Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45

Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
 140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu

	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507  
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 ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150  
 tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
 cgccctgcgg tgtcccgagg gctgaggtct cctcatcttc tccctagcag 250  
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 cagcctacc ggcccggccg tagggtgtgt gctgtccggg ctcacgggga 600  
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cctgcgacgg gcaccggggcc tgcagcacct accgaaccat ctataggacc 700  
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cccttcctcg ggaggctccc cagaccctgg catgggatgg gctgggatct 1500  
 tctctgtgaa tccaccctg gctaccccca cctgggtac cccaacggca 1550  
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<210> 508

<211> 273

<212> PRT

<213> Homo sapiens

<400> 508

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45



Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60

Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75

Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90

Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105

Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120

Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135

Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150

Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165

Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180

Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195

Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala  
215 220 225

Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu  
230 235 240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 509

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gcggccacca tggccacgcc tggggtccag cagcatcagc agcccccagg 200  
accggggagg cacaggtggc cccaccacc cggaggagca gtcctgccc 250  
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gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650  
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cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750  
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actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtaactc 850  
~~tgtgtgcccc-agggagggcc-ccccagggtg-gcccccaacc-cgacaggagt 900~~

ggacagtgc atgaaggaa aagtgcagag gctgcagtcc aggggtggacc 950  
tgctggagga gaagctgcag ctggtgctgg cccactgca cagcctggcc 1000  
tcgaggcac tggagcatgg gtcgccgac cccggcagcc tcttggtgca 1050  
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gtgggccctc agctgaggga aggtacgagc tccctgctgg agcctgggac 1450  
ccatggcaca ggccaggcag cccggaggct ggggtgggcc tcagtggggg 1500

ctgctgcctg acccccagca caataaaaaat gaaacgtg 1538

<210> 510  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 510

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30

Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60

Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75

Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90

Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105

Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120

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Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135

Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150

Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165

Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly
				170					175					180

Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala
				185					190					195

Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu
				200					205					210

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225

Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu  
245 250 255

Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys  
260 265 270

Lys Asp Ser

<210> 511  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 511  
tggagcagca atatgccagc c 21

<210> 512  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 512  
tcttcactc ctgtcgggtt gg 22

<210> 513  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 513  
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
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ggagacagcc tcccggcccc gggaggacaa gtcgctgcca cctttggctg 100

ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150  
agttgggtct ccgtgtttca ggccggctcc cccttcctgg tctcccttct 200  
cccgtgggc cggtttatcg ggaggagatt gtcttcagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350  
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<210> 515

<211> 364

<212> PRT

<213> Homo sapiens

<400> 515

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Met	Ala	Arg	Gln	Lys	Gly	Ile	Phe	Tyr	Leu	Thr	Leu	Phe	Leu	Ile					
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Leu	Gly	Thr	Cys	Thr	Leu	Phe	Phe	Ala	Phe	Glu	Cys	Arg	Tyr	Leu					
				50					55					60					
Ala	Val	Gln	Leu	Ser	Pro	Ala	Ile	Pro	Val	Phe	Ala	Ala	Met	Leu					
				65					70					75					
Phe	Leu	Phe	Ser	Met	Ala	Thr	Leu	Leu	Arg	Thr	Ser	Phe	Ser	Asp					
				80					85					90					
Pro	Gly	Val	Ile	Pro	Arg	Ala	Leu	Pro	Asp	Glu	Ala	Ala	Phe	Ile					
				95					100					105					
Glu	Met	Glu	Ile	Glu	Ala	Thr	Asn	Gly	Ala	Val	Pro	Gln	Gly	Gln					
				110					115					120					
Arg	Pro	Pro	Pro	Arg	Ile	Lys	Asn	Phe	Gln	Ile	Asn	Asn	Gln	Ile					
				125					130					135					
Val	Lys	Leu	Lys	Tyr	Cys	Tyr	Thr	Cys	Lys	Ile	Phe	Arg	Pro	Pro					
				140					145					150					
Arg	Ala	Ser	His	Cys	Ser	Ile	Cys	Asp	Asn	Cys	Val	Glu	Arg	Phe					
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Asp	His	His	Cys	Pro	Trp	Val	Gly	Asn	Cys	Val	Gly	Lys	Arg	Asn					
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<del>Tyr</del>	<del>Arg</del>	<del>Tyr</del>	<del>Phe</del>	<del>Tyr</del>	<del>Leu</del>	<del>Phe</del>	<del>Ile</del>	<del>Leu</del>	<del>Ser</del>	<del>Leu</del>	<del>Ser</del>	<del>Leu</del>	<del>Leu</del>	<del>Thr</del>					
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Ile	Tyr	Val	Phe	Ala	Phe	Asn	Ile	Val	Tyr	Val	Ala	Leu	Lys	Ser					
				200					205					210					
Leu	Lys	Ile	Gly	Phe	Leu	Glu	Thr	Leu	Lys	Glu	Thr	Pro	Gly	Thr					
				215					220					225					
Val	Leu	Glu	Val	Leu	Ile	Cys	Phe	Phe	Thr	Leu	Trp	Ser	Val	Val					
				230					235					240					
Gly	Leu	Thr	Gly	Phe	His	Thr	Phe	Leu	Val	Ala	Leu	Asn	Gln	Thr					
				245					250					255					
Thr	Asn	Glu	Asp	Ile	Lys	Gly	Ser	Trp	Thr	Gly	Lys	Asn	Arg	Val					
				260					265					270					
Gln	Asn	Pro	Tyr	Ser	His	Gly	Asn	Ile	Val	Lys	Asn	Cys	Cys	Glu					
				275					280					285					
Val	Leu	Cys	Gly	Pro	Leu	Pro	Pro	Ser	Val	Leu	Asp	Arg	Arg	Gly					
				290					295					300					
Ile	Leu	Pro	Leu	Glu	Glu	Ser	Gly	Ser	Arg	Pro	Pro	Ser	Thr	Gln					

	305		310		315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
	335		340		345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
	350		355		360
Glu Ala Glu Lys					

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
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 <223> unknown base

<400> 516  
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 tttggctttg gactctcnct ttctcccaca gacncttcg accatcactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcacctt ttntctctcc cncctcaca tctatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 517  
 caacgtgatt tcaaagctgg gctc 24

<210> 518  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 518



gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

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<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

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<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

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caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150

aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200

tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300

gtgcactatt gacaaccggg tcaccggggt ggctggcta aaccgcagca 350

ccatcctcta tgctgggaat gacaagtggg gctggatcc tcgctgggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450  
tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
caaagacctc taggggtccac ctcatgtgac aagtatctcc caaaattgta 550  
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<210> 523

<211> 344

<212> PRT

<213> Homo sapiens

<400> 523

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Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro  
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Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
35 40 45

Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
50 55 60

Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
65 70 75

Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
80 85 90

Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
95 100 105

Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
110 115 120

Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
125 130 135

Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
140 145 150

Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
155 160 165

Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
170 175 180

Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
185 190 195

Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
200 205 210

Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
215 220 225

Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr  
230 235 240

Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp  
245 250 255

Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys  
260 265 270

Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val  
275 280 285

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys  
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala  
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val  
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe  
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<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500

gag 503

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<212> DNA

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cctccagcag agccccacc attcactgtg acatctttcc gtgtcacct 2550  
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 cc 2602

<210> 526  
 <211> 736  
 <212> PRT  
 <213> Homo sapiens

<400> 526  
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 Glu Leu Val Leu Ala Gly Ala Ser Leu Leu Leu Ala Ala Leu Leu  
 35 40 45  
 Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro  
 50 55 60

Ser His Ser Thr Cys Leu Thr Glu Ala Cys Ile Arg Val Ala Gly  
65 70 75

Lys Ile Leu Glu Ser Leu Asp Arg Gly Val Ser Pro Cys Glu Asp  
80 85 90

Phe Tyr Gln Phe Ser Cys Gly Gly Trp Ile Arg Arg Asn Pro Leu  
95 100 105

Pro Asp Gly Arg Ser Arg Trp Asn Thr Phe Asn Ser Leu Trp Asp  
110 115 120

Gln Asn Gln Ala Ile Leu Lys His Leu Leu Glu Asn Thr Thr Phe  
125 130 135

Asn Ser Ser Ser Glu Ala Glu Gln Lys Thr Gln Arg Phe Tyr Leu  
140 145 150

Ser Cys Leu Gln Val Glu Arg Ile Glu Glu Leu Gly Ala Gln Pro  
155 160 165

Leu Arg Asp Leu Ile Glu Lys Ile Gly Gly Trp Asn Ile Thr Gly  
170 175 180

Pro Trp Asp Gln Asp Asn Phe Met Glu Val Leu Lys Ala Val Ala  
185 190 195

Gly Thr Tyr Arg Ala Thr Pro Phe Phe Thr Val Tyr Ile Ser Ala  
200 205 210

Asp Ser Lys Ser Ser Asn Ser Asn Val Ile Gln Val Asp Gln Ser  
215 220 225

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Gly Leu Phe Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Arg Thr Ala  
230 235 240

Asn Glu Lys Val Leu Thr Ala Tyr Leu Asp Tyr Met Glu Glu Leu  
245 250 255

Gly Met Leu Leu Gly Gly Arg Pro Thr Ser Thr Arg Glu Gln Met  
260 265 270

Gln Gln Val Leu Glu Leu Glu Ile Gln Leu Ala Asn Ile Thr Val  
275 280 285

Pro Gln Asp Gln Arg Arg Asp Glu Glu Lys Ile Tyr His Lys Met  
290 295 300

Ser Ile Ser Glu Leu Gln Ala Leu Ala Pro Ser Met Asp Trp Leu  
305 310 315

Glu Phe Leu Ser Phe Leu Leu Ser Pro Leu Glu Leu Ser Asp Ser  
320 325 330

Glu Pro Val Val Val Tyr Gly Met Asp Tyr Leu Gln Gln Val Ser  
335 340 345

Glu Leu Ile Asn Arg Thr Glu Pro Ser Ile Leu Asn Asn Tyr Leu  
350 355 360

Ile Trp Asn Leu Val Gln Lys Thr Thr Ser Ser Leu Asp Arg Arg  
365 370 375

Phe Glu Ser Ala Gln Glu Lys Leu Leu Glu Thr Leu Tyr Gly Thr  
380 385 390

Lys Lys Ser Cys Val Pro Arg Trp Gln Thr Cys Ile Ser Asn Thr  
395 400 405

Asp Asp Ala Leu Gly Phe Ala Leu Gly Ser Leu Phe Val Lys Ala  
410 415 420

Thr Phe Asp Arg Gln Ser Lys Glu Ile Ala Glu Gly Met Ile Ser  
425 430 435

Glu Ile Arg Thr Ala Phe Glu Glu Ala Leu Gly Gln Leu Val Trp  
440 445 450

Met Asp Glu Lys Thr Arg Gln Ala Ala Lys Glu Lys Ala Asp Ala  
455 460 465

Ile Tyr Asp Met Ile Gly Phe Pro Asp Phe Ile Leu Glu Pro Lys  
470 475 480

Glu Leu Asp Asp Val Tyr Asp Gly Tyr Glu Ile Ser Glu Asp Ser  
485 490 495

Phe Phe Gln Asn Met Leu Asn Leu Tyr Asn Phe Ser Ala Lys Val  
500 505 510

Met Ala Asp Gln Leu Arg Lys Pro Pro Ser Arg Asp Gln Trp Ser  
515 520 525

Met Thr Pro Gln Thr Val Asn Ala Tyr Tyr Leu Pro Thr Lys Asn  
530 535 540

Glu Ile Val Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Ala  
545 550 555

Arg Asn His Pro Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val  
560 565 570

Met Gly His Glu Leu Thr His Ala Phe Asp Asp Gln Gly Arg Glu  
575 580 585

Tyr Asp Lys Glu Gly Asn Leu Arg Pro Trp Trp Gln Asn Glu Ser  
590 595 600

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Asn Gln Tyr Gln Val Asn Gly Glu Arg Leu Asn Gly Arg Gln Thr  
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<210> 579

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 579

aagcttctgt tcaatcccag cgggcc 26

<210> 580

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 580

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<210> 581

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 581

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<210> 582

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<220>

<223> Synthetic oligonucleotide probe

<400> 582

acacctgagg cacctgagag aggaactct 29



<210> 583  
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<210> 585  
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cacaactgct gaccccgccc a 21

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<210> 586  
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<400> 586  
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<210> 589  
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<400> 589  
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<210> 590  
<211> 21  
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<400> 590  
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<210> 591  
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<210> 592  
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<400> 592  
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<210> 593  
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<400> 593  
ctttgaatag aagacttctg gacaattt 28

<210> 594  
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<400> 598

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<210> 599

<211> 20

<212> DNA

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<223> Synthetic oligonucleotide probe

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<210> 600

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 600

gactacaagg cgctcagcta 20

<210> 601

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 601

ccggctgggt ctcaactcctc c 21

<210> 602

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 602

cgttcgtgca gcgtgtgta 19

<210> 603

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<210> 605  
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<400> 605  
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<210> 606  
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<400> 607  
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<210> 608  
<211> 19  
<212> DNA  
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<400> 608  
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<210> 609  
<211> 25  
<212> DNA  
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<400> 609  
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<210> 610  
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<220>  
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<210> 611  
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aacaacaccc aacaactggg gtggggggaa gaaagaaaga aaagaaaccc-150  
accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200  
ctgtggcgcg ccgcctggtt cccgggaaga ctcgccagca ccagggggtg 250  
ggggagtgcg agctgaaagc tgctggagag tgagcagccc tagcagggat 300  
ggacatgatg ctgttggtgc aggggtgctt ttgctcgaac cagtggctgg 350  
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ggacagagtg tggacttccc ctgggcggcc gtggacaaca tgatggtcag 450  
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aattactttt agaggatatt aattgtgatt tcatgtttgt aatctacaac 1650  
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 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612

<211> 352

<212> PRT

<213> Homo Sapien

<400> 612

Met	Met	Leu	Leu	Val	Gln	Gly	Ala	Cys	Cys	Ser	Asn	Gln	Trp	Leu
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Ala	Ala	Val	Leu	Leu	Ser	Leu	Cys	Cys	Leu	Leu	Pro	Ser	Cys	Leu
				20					25					30
Pro	Ala	Gly	Gln	Ser	Val	Asp	Phe	Pro	Trp	Ala	Ala	Val	Asp	Asn
				35					40					45
Met	Met	Val	Arg	Lys	Gly	Asp	Thr	Ala	Val	Leu	Arg	Cys	Tyr	Leu
				50					55					60
Glu	Asp	Gly	Ala	Ser	Lys	Gly	Ala	Trp	Leu	Asn	Arg	Ser	Ser	Ile
				65					70					75
Ile	Phe	Ala	Gly	Gly	Asp	Lys	Trp	Ser	Val	Asp	Pro	Arg	Val	Ser
				80					85					90
Ile	Ser	Thr	Leu	Asn	Lys	Arg	Asp	Tyr	Ser	Leu	Gln	Ile	Gln	Asn
				95					100					105
Val	Asp	Val	Thr	Asp	Asp	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr



110	115	120
Gln His Thr Pro Arg Thr Met Gln Val	His Leu Thr Val Gln Val	
125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
335	340	345
Leu Lys Asn Ala Ile Leu Gln		
350		

<210> 613

<211> 1797

<212> DNA

<213> Homo Sapien

<400> 613

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aaataagaaa atttctcaagg aggacgagct cttgagttag acccaacaag 150  
ctgcttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250  
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ctggcgggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400  
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cccagggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600  
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gatggagcaa caggccctc gggaccccaa ggcccaccgg gagtcaaggg 700  
agaggcgggc ctccaaggac ccagggtgc tccagggaag caaggagcca 750  
ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
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~~gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcagggg 900~~

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acctggactg caggggtgtc cgggccctcc tggtagcagt ggacaccag 1050  
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ccaggagacc ccgggagtc aggagccaca ggcctgaaag gaagcaaagg 1150  
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagttc 1200  
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cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300  
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aaaactcagt gtccgtcagg attgtcggca gtagtaaccg aggccgggct 1400  
gaagtttact acagtggtag ctgggggaca atttgcgatg acgagtggca 1450

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 gcgtctgacc cggaaaccct ttcacttctc tgctcccagag gtgtcctcgg 1700  
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<210> 614  
 <211> 520  
 <212> PRT  
 <213> Homo Sapien

<400> 614

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Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45	
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60	
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75	
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90	
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105	
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120	
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135	
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150	
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165	
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180	
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln				

185										190					195				
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln					
				200					205					210					
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln					
				215					220					225					
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys					
				230					235					240					
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro					
				245					250					255					
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met					
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Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro					
				275					280					285					
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln					
				290					295					300					
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val					
				305					310					315					
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro					
				320					325					330					
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr					
				335					340					345					
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln					
				350					355					360					
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys					
				365					370					375					
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro					
				380					385					390					
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser					
				395					400					405					
Gly	Glu	Gln	Gly	Val	Lys	Gly	Glu	Lys	Gly	Glu	Arg	Gly	Glu	Asn					
				410					415					420					
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala					
				425					430					435					
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Glu					
				440					445					450					
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr					
				455					460					465					
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln					

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

<210> 615  
 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
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 atttaagaag catcctctgc caagaccaa aggaaagaag aaaaagggcc 150  
 aaaagccaaa atgaaactga tggctactgt tttcaccatt gggctaactt 200  
 tgctgctagg agttcaagcc atgcctgcaa atcgctctc ttgctacaga 250  
 aagatactaa aagatcacaa ctgtcacaa cttccggaag gagtagctga 300  
 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400  
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 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500  
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550  
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaattctgt 600  
 gttaaacaag tagtaataaa agttaattca atctaaaaa aaaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
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 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
				80					85					90
Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
				95										

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617  
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 accccgccgt ggtggttggg gggcgcgag tagagcagca gcacaggcgc 150  
 gggccccggg aggccggctc tgctcgcgcc gagatgtgga atctccttca 200  
 cgaaaccgac tgggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250  
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg ctctcctctc 300  
 ggtgtgttta taaaatcctc caatgaagct actaacatta ctcaaagca 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450  
 tttcagcttg caaagcaa atcaatccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
 ctcatcccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600  
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcgga 650  
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggag 700  
 atctagtgtg tgtaactat gcacgaactg aagacttctt taaattggaa 750  
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800  
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cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050  
ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100  
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tcaaagtgcc ctacaatggt ggacctggct ttactggaaa cttttctaca 1200  
caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350  
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acctcactgt ggcccagggt cgaggaggga tgggtgttga gctagccaat 1950  
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 gaatccgtat tgaatttggtg tggtatgtca ctcagaaaga atcgtaatgg 2500  
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<210> 618  
 <211> 750  
 <212> PRT  
 <213> Homo Sapien

<400> 618  
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 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly  
 20 25 30  
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser  
 35 40 45  
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala  
 50 55 60  
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His  
 65 70 75  
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe  
 80 85 90  


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 Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu  
 95 100 105  
 Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro  
 110 115 120  
 Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly  
 125 130 135  
 Asn Glu Ile Phe Asn Thr Ser Leu Phe Glu Pro Pro Pro Pro Gly  
 140 145 150  
 Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser  
 155 160 165  
 Pro Gln Gly Met Pro Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala  
 170 175 180  
 Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn  
 185 190 195  
 Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg  
 200 205 210



Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	Gln Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
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Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Glu	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Pro	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro	
				500					505					510	
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe	
				515					520					525	
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn	
				530					535					540	
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val	
				545					550					555	
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	
				560					565					570	
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	
				575					580					585	
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr	
				590					595					600	
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser	
				605					610					615	
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp	
				620					625					630	
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys	
				635					640					645	
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val	
				650					655					660	
<del>Leu</del>	<del>Arg</del>	<del>Met</del>	<del>Met</del>	<del>Asn</del>	<del>Asp</del>	<del>Gln</del>	<del>Leu</del>	<del>Met</del>	<del>Phe</del>	<del>Leu</del>	<del>Glu</del>	<del>Arg</del>	<del>Ala</del>	<del>Phe</del>	
				665					670					675	
Ile	Asp	Pro	Leu	Gly	Leu	Pro	Asp	Arg	Pro	Phe	Tyr	Arg	His	Val	
				680					685					690	
Ile	Tyr	Ala	Pro	Ser	Ser	His	Asn	Lys	Tyr	Ala	Gly	Glu	Ser	Phe	
				695					700					705	
Pro	Gly	Ile	Tyr	Asp	Ala	Leu	Phe	Asp	Ile	Glu	Ser	Lys	Val	Asp	
				710					715					720	
Pro	Ser	Lys	Ala	Trp	Gly	Glu	Val	Lys	Arg	Gln	Ile	Tyr	Val	Ala	
				725					730					735	
Ala	Phe	Thr	Val	Gln	Ala	Ala	Ala	Glu	Thr	Leu	Ser	Glu	Val	Ala	
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<210> 619

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

agatgtgaag gtgcaggtgt gccg 24

<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccgta attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 621

ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tgggaaatca ggaatggtgt tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide probe

<400> 624

cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50